Network Systems Science & Advanced Computing

Biocomplexity Institute & Initiative

University of Virginia

Estimation of COVID-19 Impact in Virginia

March 3rd, 2021

(data current to March 1st-2nd)

Biocomplexity Institute Technical report: TR 2021-024

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About Us

- Biocomplexity Institute at the University of Virginia
  - Using big data and simulations to understand massively interactive systems and solve societal problems
- Over 20 years of crafting and analyzing infectious disease models
  - Pandemic response for Influenza, Ebola, Zika, and others

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Overview

- **Goal**: Understand impact of COVID-19 mitigations in Virginia
- **Approach:**
  - Calibrate explanatory mechanistic model to observed cases
  - Project based on scenarios for next 4 months
  - Consider a range of possible mitigation effects in "what-if" scenarios
- **Outcomes:**
  - Ill, Confirmed, Hospitalized, ICU, Ventilated, Death
  - Geographic spread over time, case counts, healthcare burdens

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.
Even without perfect projections, we can confidently draw conclusions:

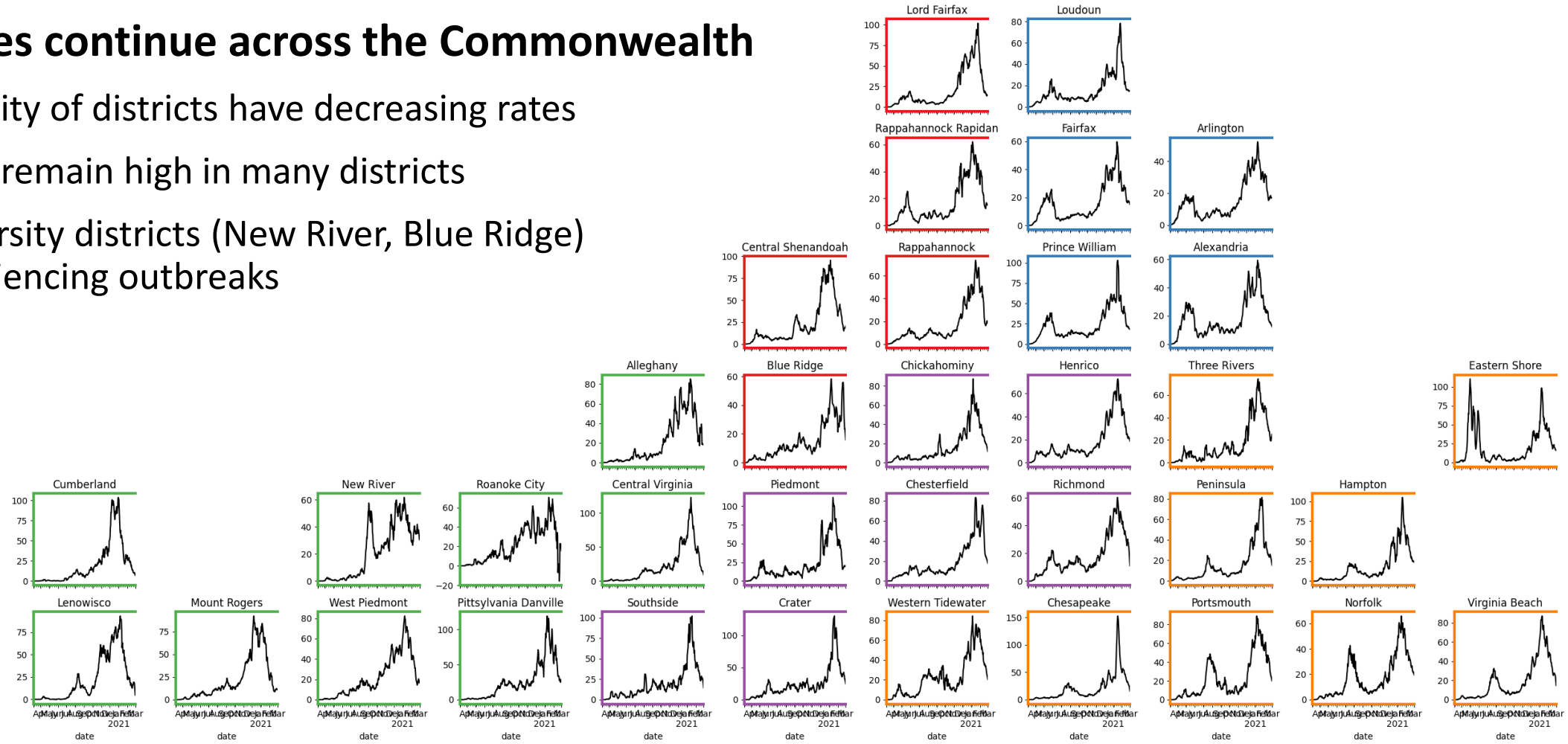
- **Case rate growth in Virginia continues to decline with a few hotspots emerging**
- VA mean weekly incidence down to 19/100K from 23/100K, US levels decline (to 18 from 19 per 100K)
- Significant progress made in last month, however 88% of VA counties above mean rate of Summer 2020
- Projections continue to be down across Commonwealth
- Recent updates:
  - Adjustment to death outcome modeling to correct for delays in reporting, higher resolution hospital data incorporated for hospital calibration
  - Ascertainment rate adjusted to better capture total infections to date
  - Further updates to vaccination schedules, with fitting now including partially vaccinated population and future vaccinations based on current levels instead of goals
- The situation is changing rapidly. Models continue to be updated regularly.

Situation Assessment

Case Rate (per 100k) by VDH District

Declines continue across the Commonwealth

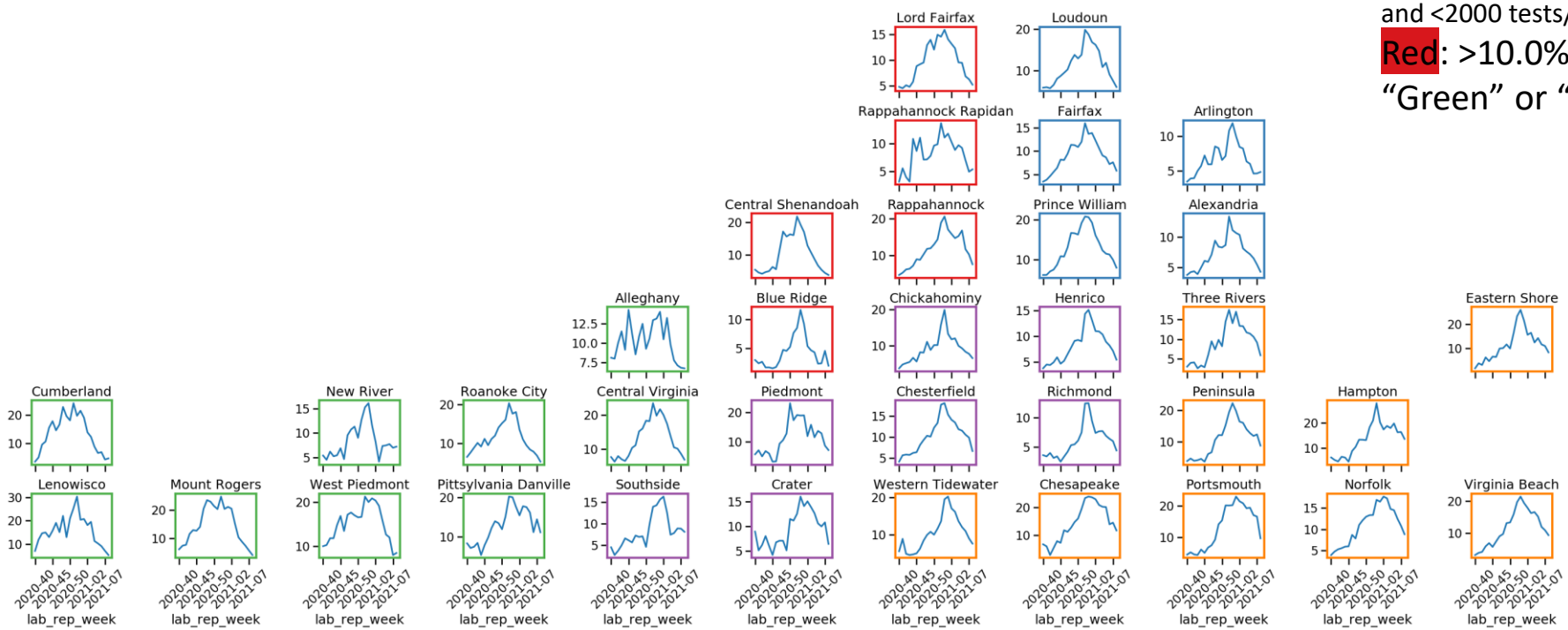
- Majority of districts have decreasing rates
- Rates remain high in many districts
- University districts (New River, Blue Ridge) experiencing outbreaks



Test Positivity by VDH District

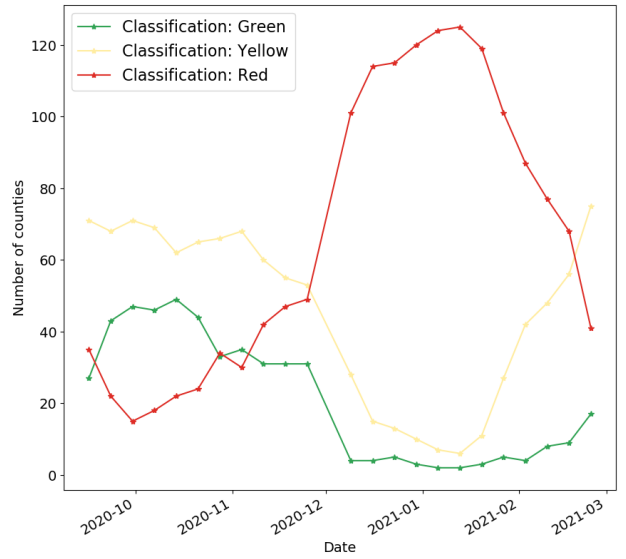
Weekly changes in test positivity by district

- Rates continue to decline
- 41 counties classified in the 'Red' category (as of Feb 24th) and are fewer than 'Yellow' for first time since late November



County level test positivity rates for RT-PCR tests.

Green: Test positivity <5.0%
(or with <20 tests in past 14 days)
Yellow: Test positivity 5.0%-10.0% (or with <500 tests and <2000 tests/100k and >10% positivity over 14 days)
Red: >10.0% and not meeting the criteria for "Green" or "Yellow"



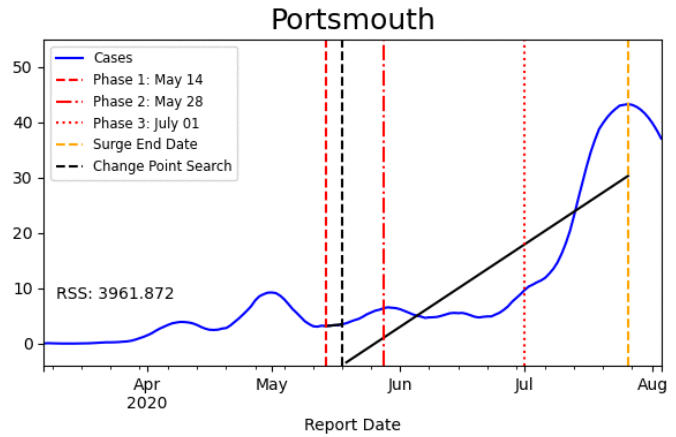
https://data.cms.gov/stories/s/q5r5-gjyu

District Trajectories

Goal: Define epochs of a Health District's COVID-19 incidence to characterize the current trajectory

Method: Find recent peak and use hockey stick fit to find inflection point afterwards, then use this period's slope to define the trajectory

Hockey stick fit

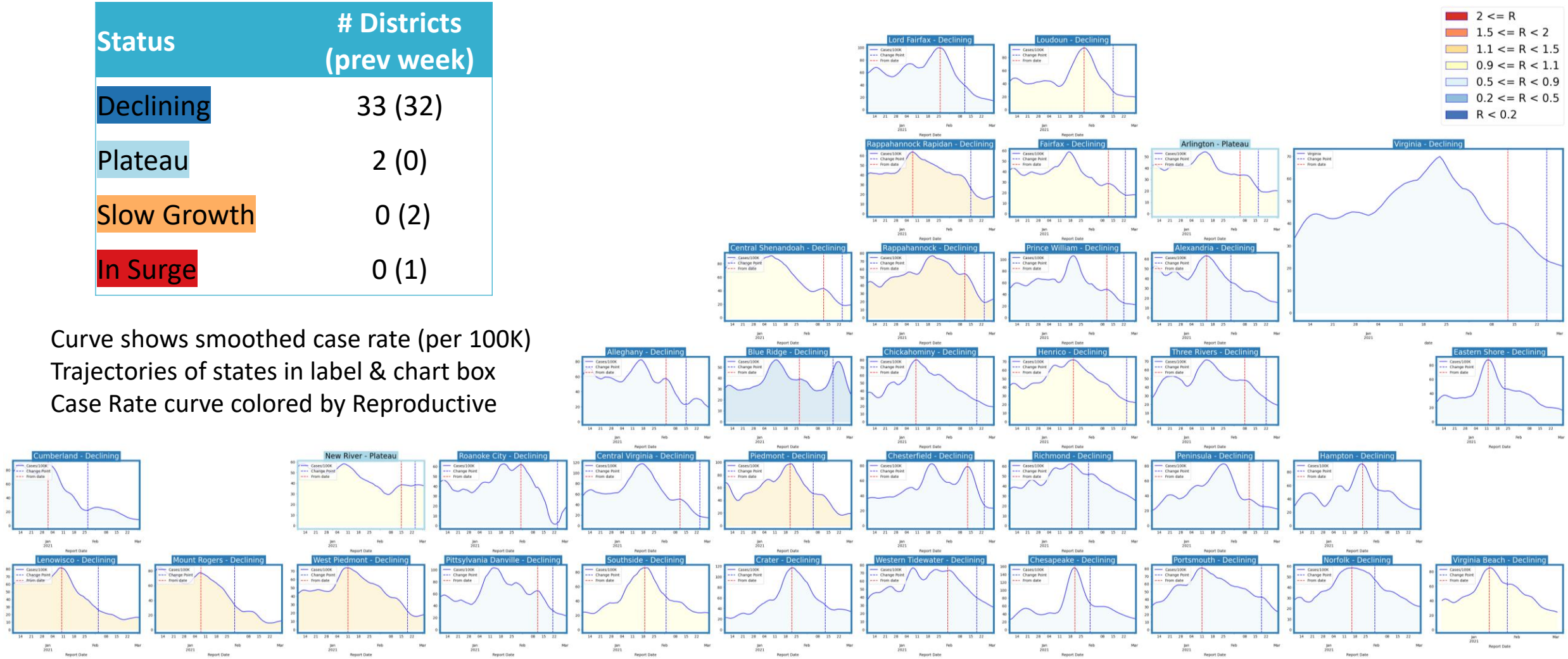


Trajectory	Description	Weekly Case Rate (per 100K) bounds	# Districts (prev week)
Declining	Sustained decreases following a recent peak	below -0.9	33 (32)
Plateau	Steady level with minimal trend up or down	above -0.9 and below 0.5	2 (0)
Slow Growth	Sustained growth not rapid enough to be considered a Surge	above 0.5 and below 2.5	0 (2)
In Surge	Currently experiencing sustained rapid and significant growth	2.5 or greater	0 (1)

District Trajectories – last 10 weeks

Status	# Districts (prev week)
Declining	33 (32)
Plateau	2 (0)
Slow Growth	0 (2)
In Surge	0 (1)

Curve shows smoothed case rate (per 100K)
Trajectories of states in label & chart box
Case Rate curve colored by Reproductive



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SARS-CoV2 Variants of Concern

Emerging new variants will alter the future trajectories of pandemic and have implications for future control

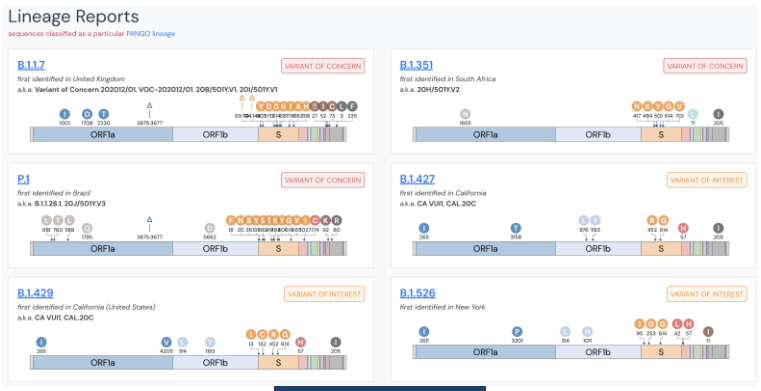
- Current evidence supports that new variants can:
  - Increase transmissibility
  - Increase severity (more hospitalizations and/or deaths)
  - Limit immunity from prior infection and vaccination
- Variants are defined by collection of co-occurring mutations that make it distinct from the other various variations in the genome.
  - Some subsets of mutations, including single amino acid substitutions, make the change that alters the virus pathogenicity

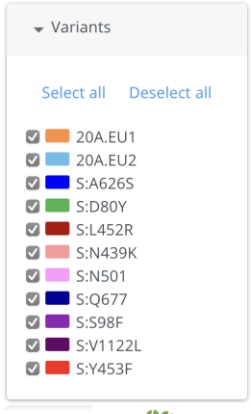
Lineages Of Concern

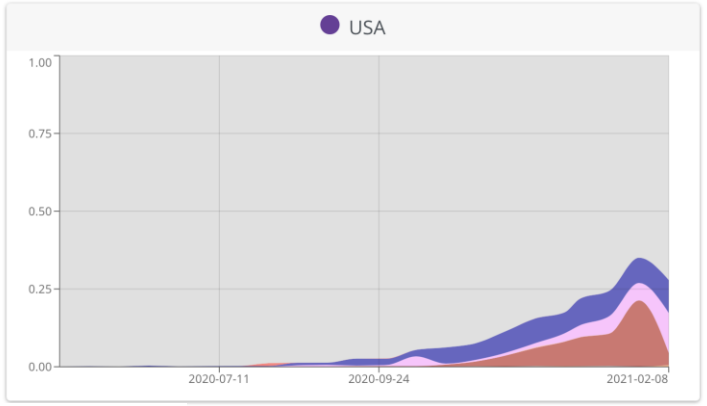
LoC name	PANGO lineage	NextStrain lineage	Other synonyms	Emergence date	Emergence location	Key AA substitutions in spike protein	Impact
B.1.1.7	B.1.1.7	20I/501Y.V1	VOC 202012/01, UK variant	September 2020	Southeast England	H69-, V70-, N501Y, D614G, P681H	Increased transmissibility; S gene target failure (SGTF)
B.1.351	B.1.351	20H/501Y.V2	South African variant	October 2020	Nelson Mandela Bay, South African	L241-, L242-, A243-, K417N, E484K, N501Y, D614G	loss of serum antibody neutralization
P.1	B.1.1.28	20J/501Y.V3	Brazilian variant	July 2020	Brazil	K417T, E484K, N501Y, D614G	Increased transmissibility; loss of serum antibody neutralization
CAL.20C	B.1.429			July 2020	Southern California, USA	W152C, L452R, D614G	loss of monoclonal antibody binding
B.1.375	B.1.375			September 2020	Massachusetts, USA	H69-, V70-, D614G	S gene target failure (SGTF)

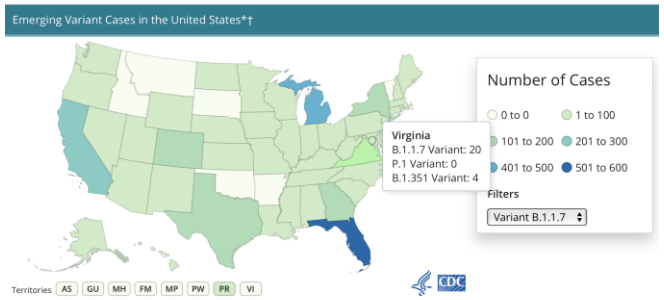
[NIH-NIAID Bacterial-Viral Bioinformatics Resource Center]

Variant	Reported Cases in US	Number of Jurisdictions Reporting
B.1.1.7	2,506	46
B.1.351	65	17
P.1	10	5







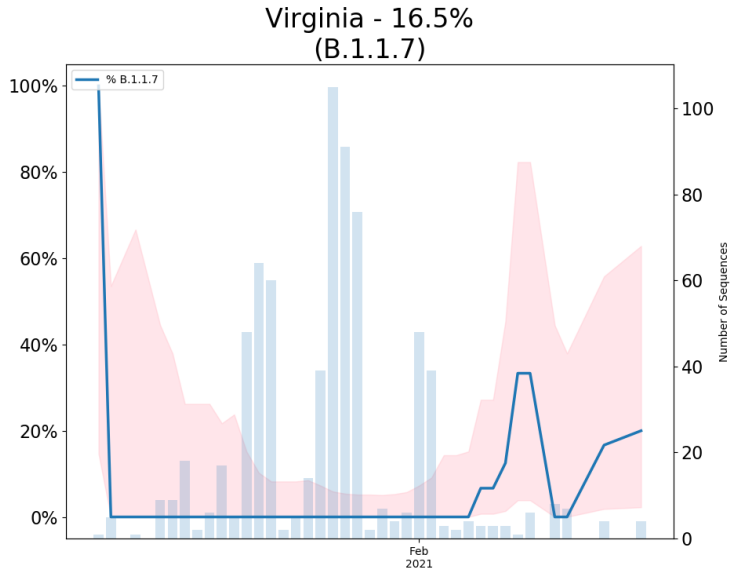


[CDC Variant Tracking]

SARS-CoV2 Variants of Concern

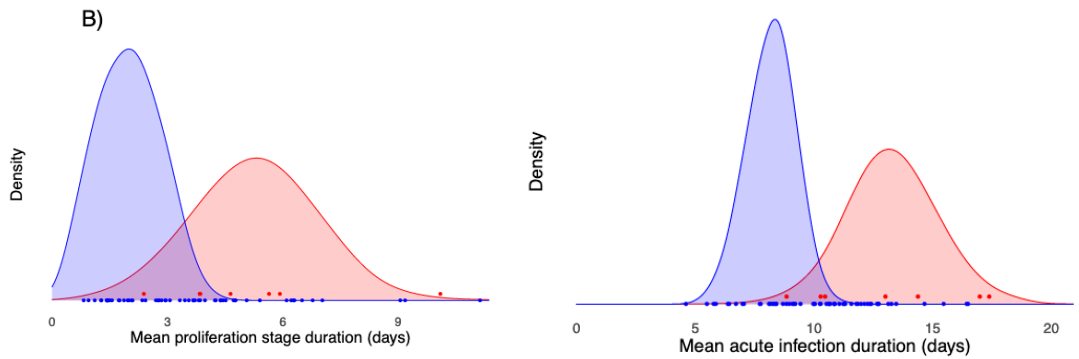
Lineage B.1.1.7

- B.1.1.7 has been detected in Virginia as well as in at least 2,506 cases across 45 states as of Mar 2nd (10-20 day delay for genotyping), will continue to grow rapidly. Current estimates place national frequency at ~10% and Virginia at 16%
- A recent study finds B.1.1.7 to have longer duration which may be the source of increased transmissibility and has implications for isolation durations
- Estimates based on US growth rates estimate it will predominate (eg reach 50% frequency) by mid to late March and is 35%-45% more transmissible
- Evidence mounts supporting increased risks of hospitalization and mortality for B.1.1.7 infected individuals



GISAID outbreak.info

Outbreak Info



Variant B.1.1.7 may cause longer infections with similar peak viral concentration compared to non-B.1.1.7 May contribute to B.1.1.7 S increased transmissibility. https://dash.harvard.edu/handle/1/37366884

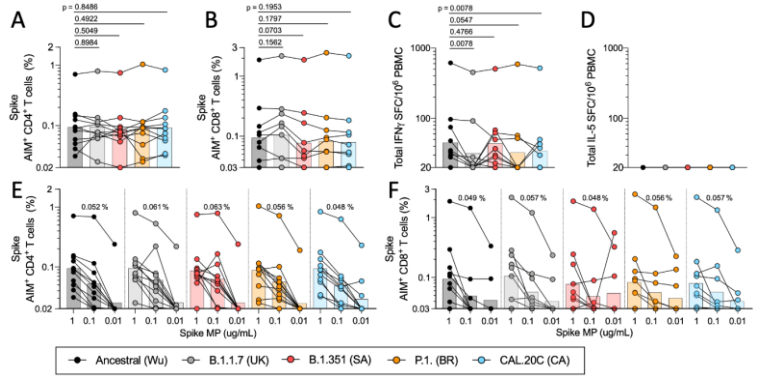
New variants of SARS-CoV2

Lineage B.1.351

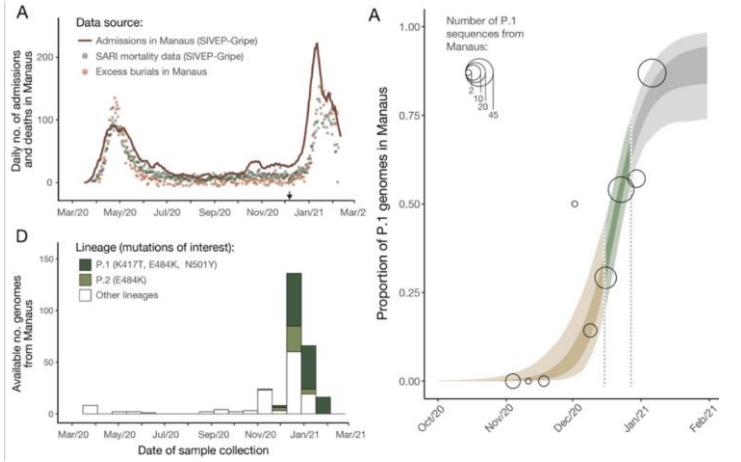
- Emerging strain initially identified in South Africa shows signs of vaccine escape, currently 46 reported cases in 14 states (including Virginia, 21 in South Carolina) as of Feb 23rd
- New study in Cell demonstrates immune escape across a bank of sera from different COVID-19 patients and vaccine recipients (Pfizer and AstraZeneca)
- Additional study demonstrates that T cell response from mRNA vaccinated individuals are not significantly degraded across these "immune escaping" variants

Additional Variants

- **Lineage P.1**: First case reported in Minnesota on Jan 25th, now at least 10 cases in 5 states caused a resurgence of hospitalizations in Manaus, Brazil and is now estimated to be 1.4-2.2 times more transmissible and able to partially evade protective immunity.
- **Lineage B.1.429 (similar mutations as in B.1.1.7 and B.1.351):** Initially found in Southern California, coincided with surge in Nov and Dec, found in over half of sequenced samples in LA
- New naming conventions in the works. May cluster these with bird names: Robin 1, Robin 2, Pelican, Yellowhammer, Mockingbird, Bluebird, Quail, etc.



Results demonstrate that CD4+ and CD8+ T cell responses in convalescent COVID-19 subjects or COVID-19 mRNA vaccinees are not substantially affected by mutations found in the SARS-CoV-2 variants

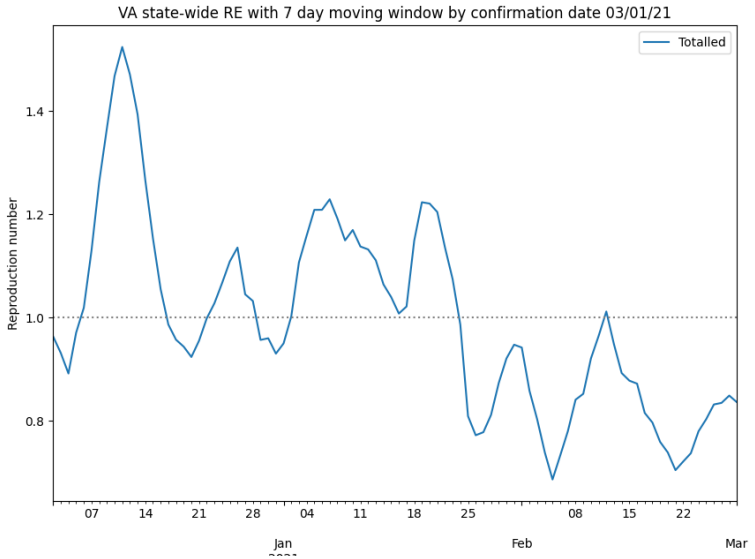


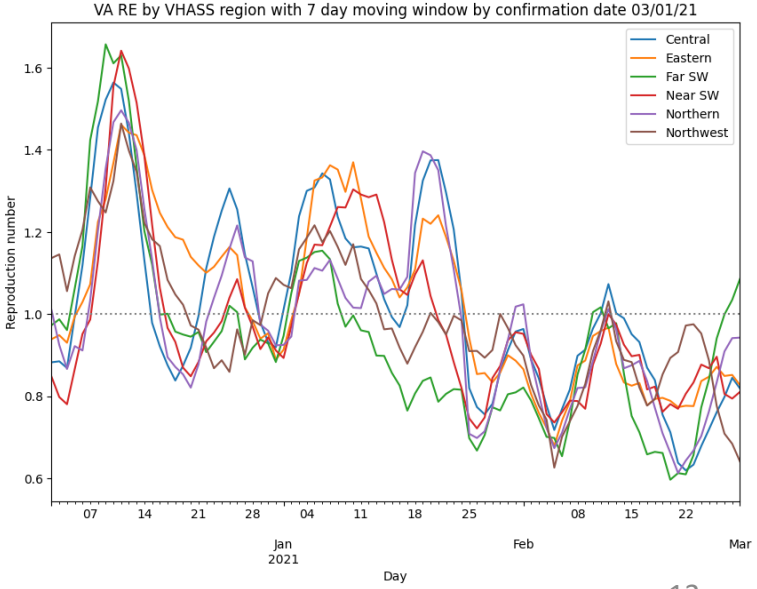
Estimate that P.1 may be 1.4–2.2 times more transmissible and able to evade 25-61% of protective immunity elicited by previous infection with non-P.1 lineages.

Estimating Daily Reproductive Number

March 1st Estimates

Region	Date Confirmed R_e	Date Confirmed Diff Last Week
State-wide	0.836	0.115
Central	0.819	0.200
Eastern	0.827	0.051
Far SW	1.085	0.476
Near SW	0.810	0.005
Northern	0.943	0.300
Northwest	0.641	-0.331





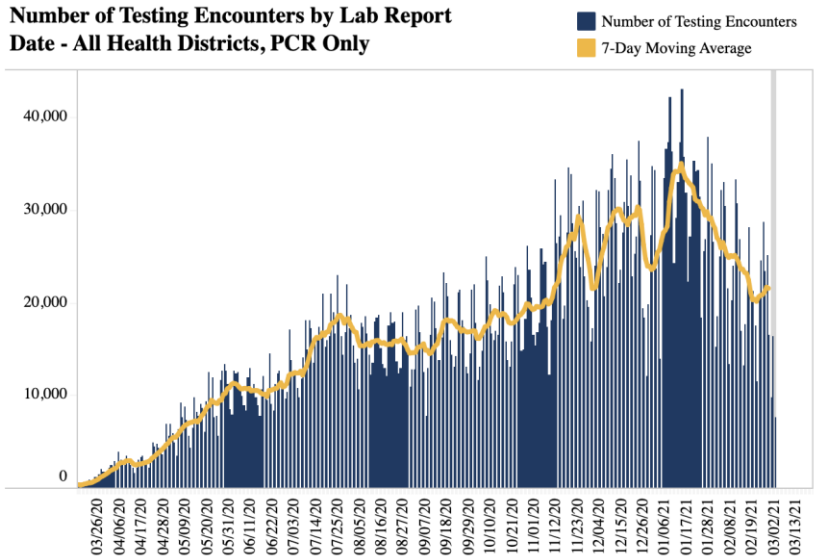
Methodology

- Wallinga-Teunis method (EpiEstim[1]) for cases by **<u>confirmation date</u>**
- Serial interval: 6 days (2 day std dev)
- Using Confirmation date since due to increasingly unstable estimates from onset date due to backfill

1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, https://doi.org/10.1093/aje/kwt133

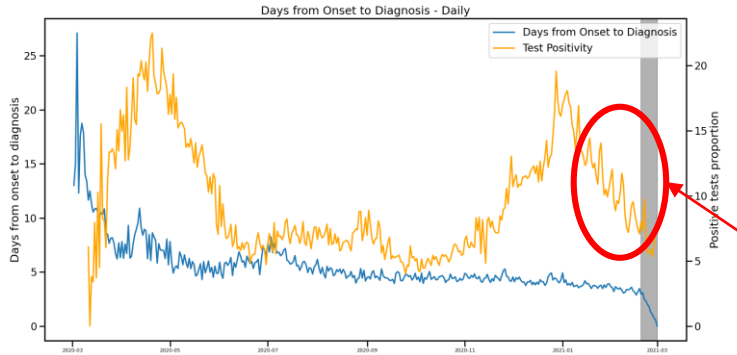
Changes in Case Detection

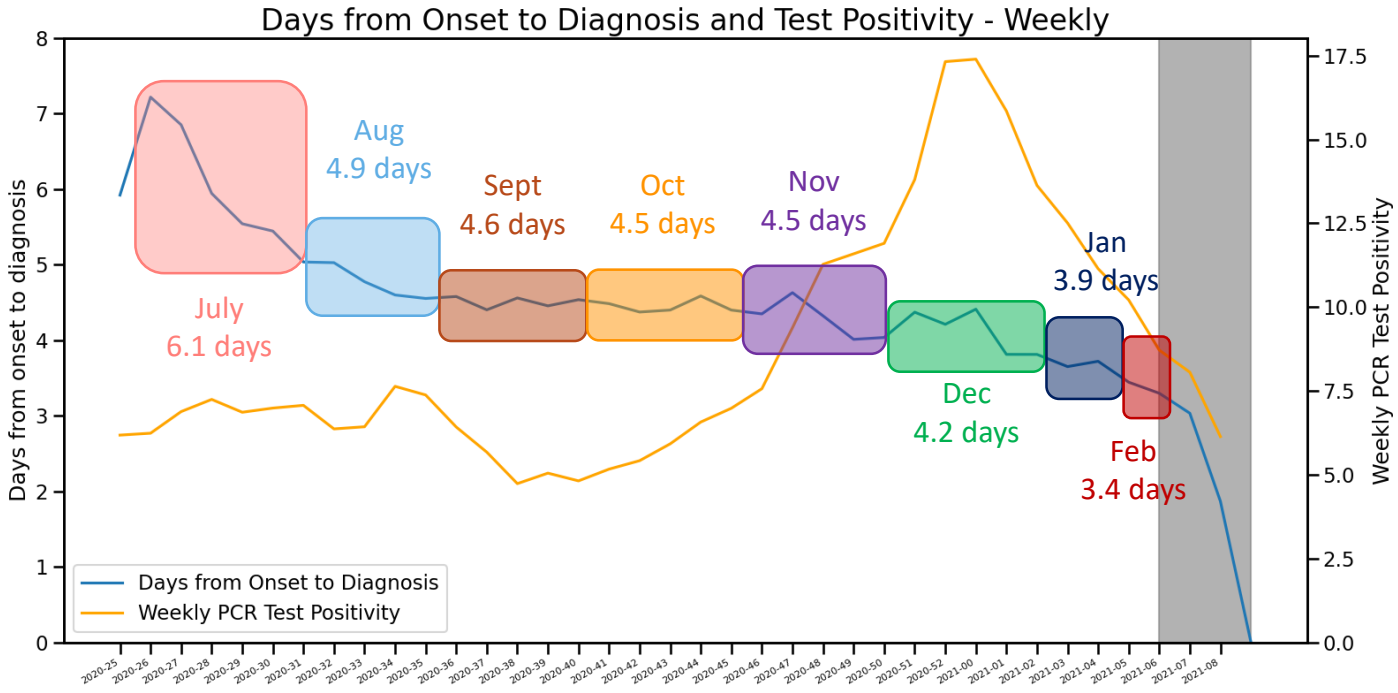
Timeframe (weeks)	Mean days	% difference from overall mean
July (26-30)	6.2	-10%
Aug (31-34)	4.9	-29%
Sept (35-38)	4.5	-34%
Oct (39-43)	4.5	-35%
Nov (44-47)	4.5	-35%
Dec (48-49)	4.2	-39%
Jan (00-04)	3.9	-43%
Feb (05-06)	3.4	-51%
Overall (13-05)	6.9	--



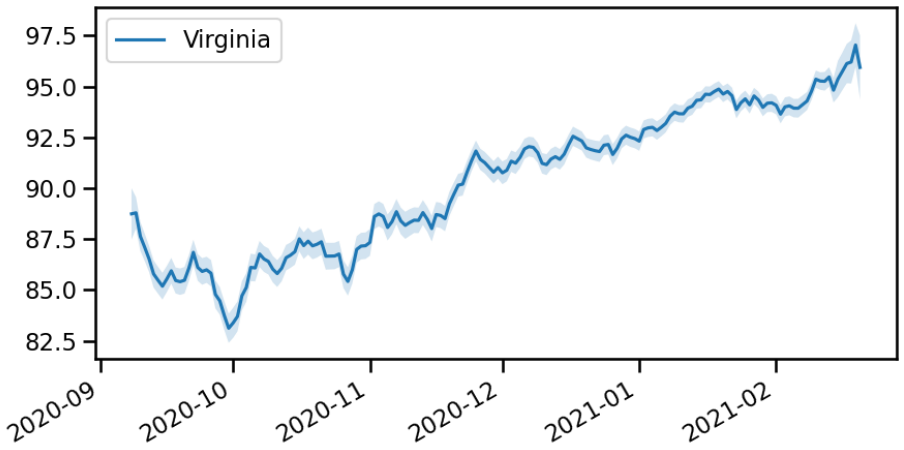
Accessed 9:00am March 3, 2021
https://www.vdh.virginia.gov/coronavirus/

Test positivity vs. Onset to Diagnosis





Mask Usage and Vaccine Acceptance in Virginia

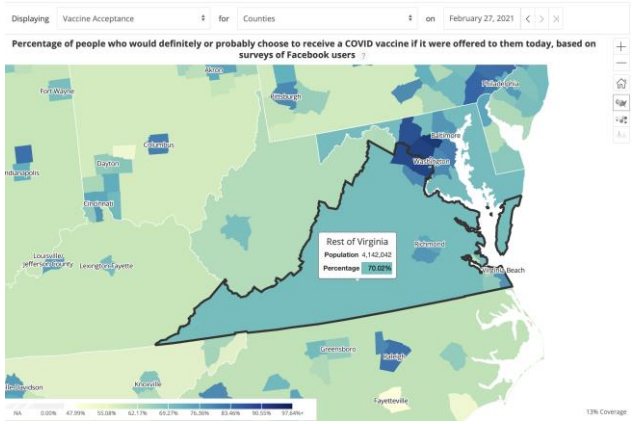


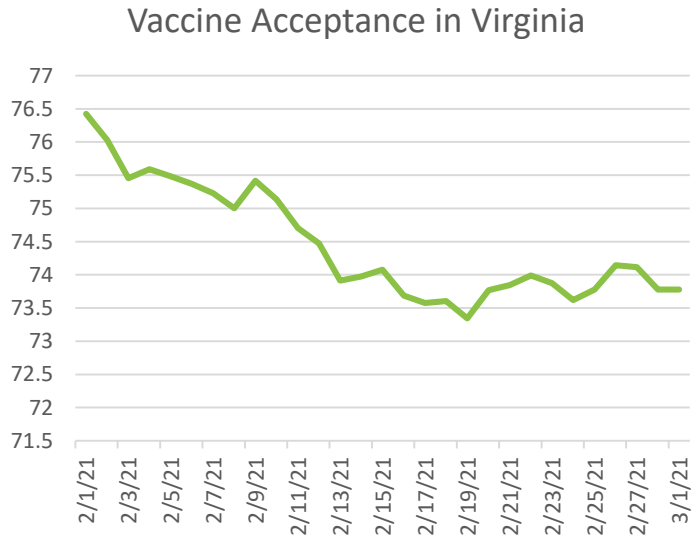
Acceptance remains high:

- Proportion of Virginians that would definitely or probably accept vaccination if offered today
- Nearly ¾ of Virginians are likely to choose to be vaccinated
- Down very slightly from high at end of January, but has been stable for several weeks
- Urban areas have slightly higher acceptance rates

Reported mask usage for Virginia remains high

- Facebook surveys have shown steady increase over past three months
- ~88% (early Nov) to ~96% (late Feb)
- Some variance across the Commonwealth
- ~3000 daily responses from VA





Data Source: https://covidcast.cmu.edu

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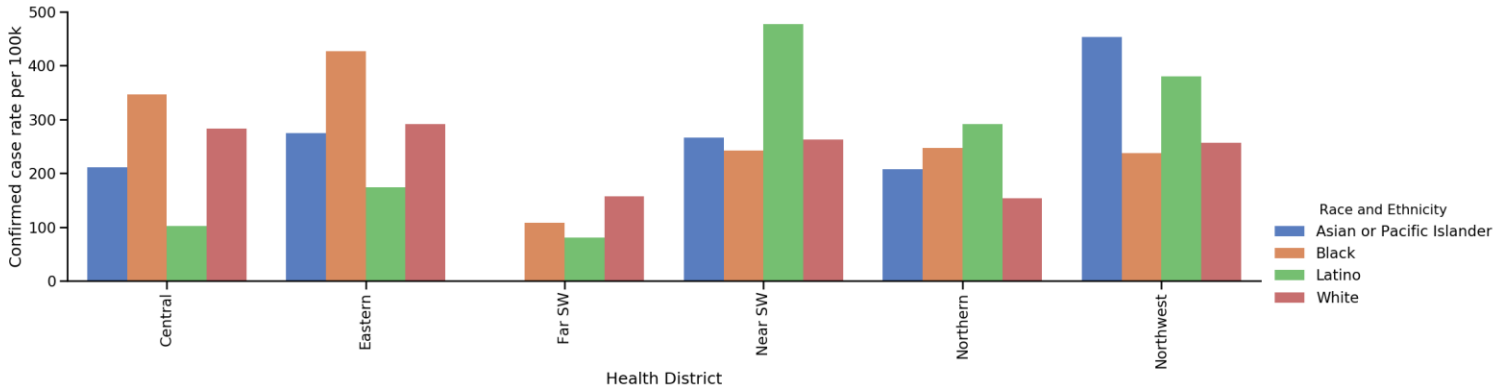
Race and Ethnicity – Recent Rate Changes (per 100K)

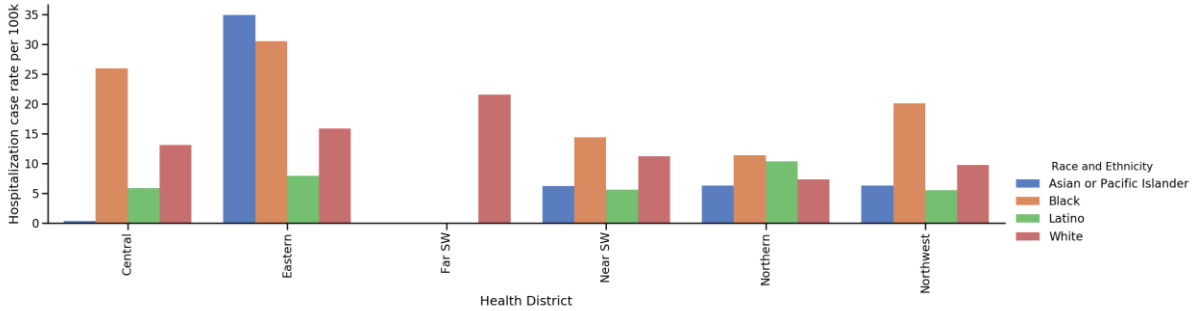
Changes in Race and Ethnicity Rates (per 100k) in past two weeks

- Two week change in population level rates
- Black, Latinx and 2 or more races populations have much higher changes in rates; disparity is more pronounced in some regions than others
- Based on 2019 census race-ethnicity data by county

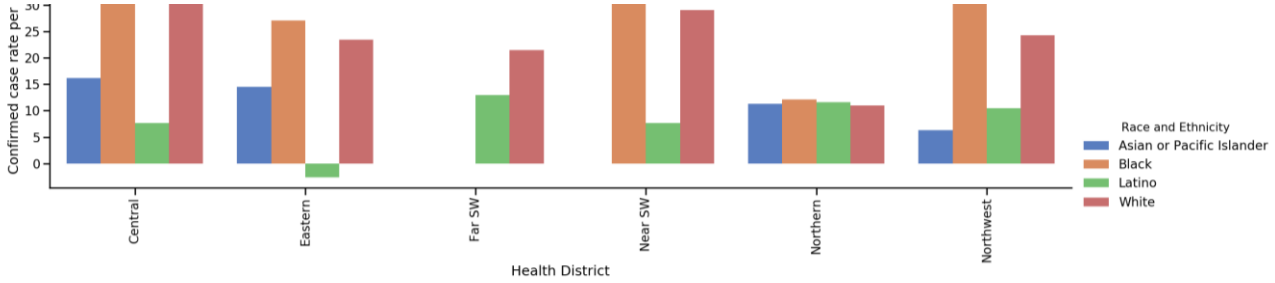
Case Rate



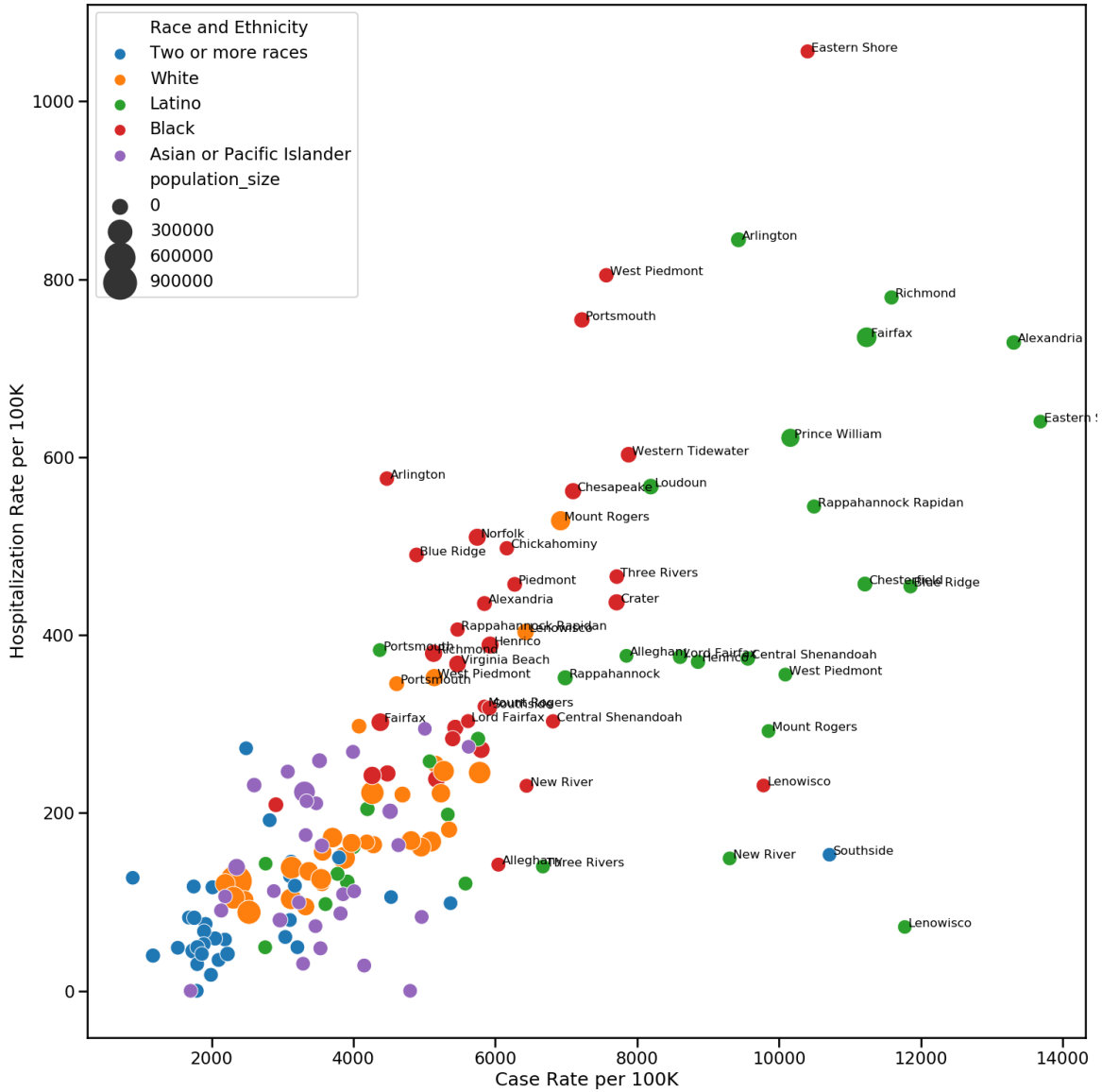
Hospitalization Rate



Death Rate



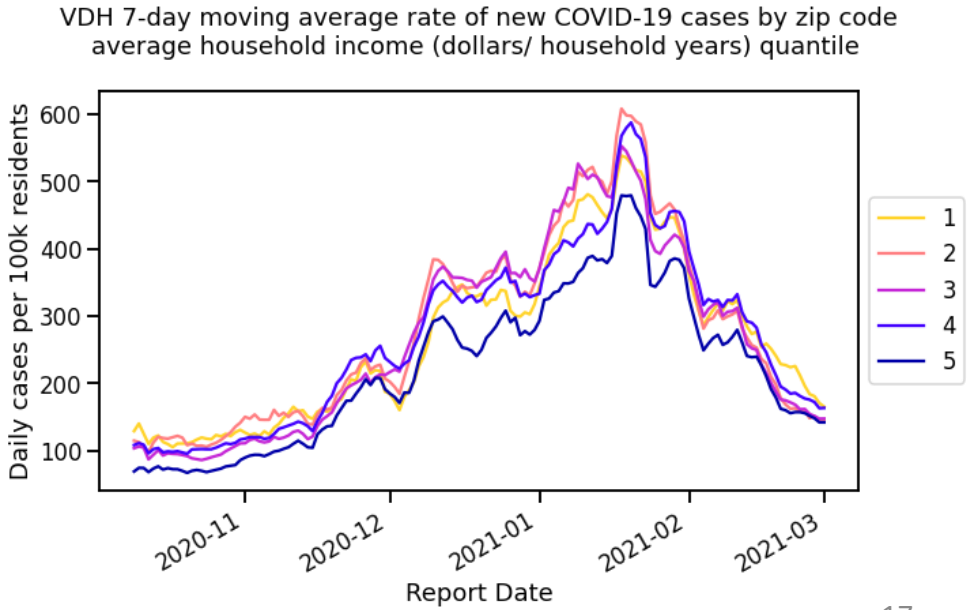
Race and Ethnicity cases per 100K



Rates per 100K of each Racial-Ethnic population by Health District

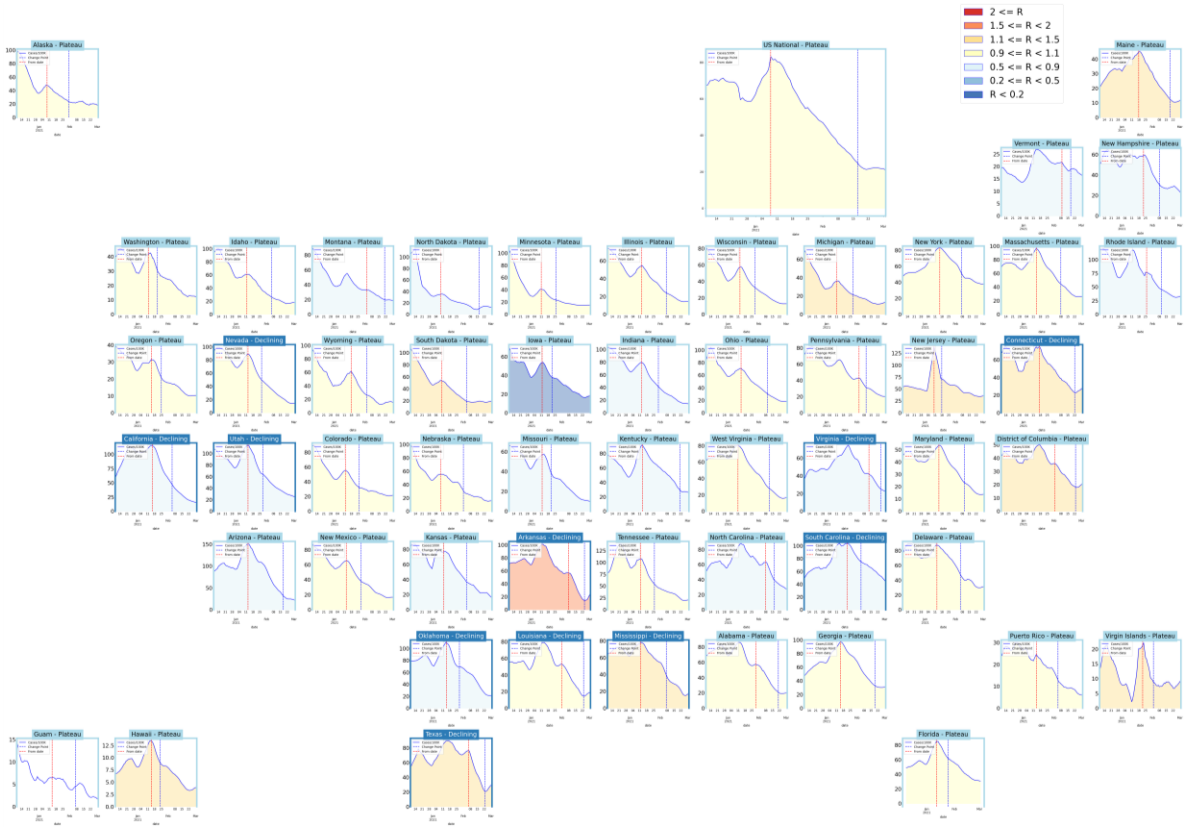
- Each Health District's Racial-Ethnic population is plotted by their Hospitalization and Case Rate
- Points are sized based on their overall population size (overlapping labels removed)

Case rates by zip codes broken into income quintiles



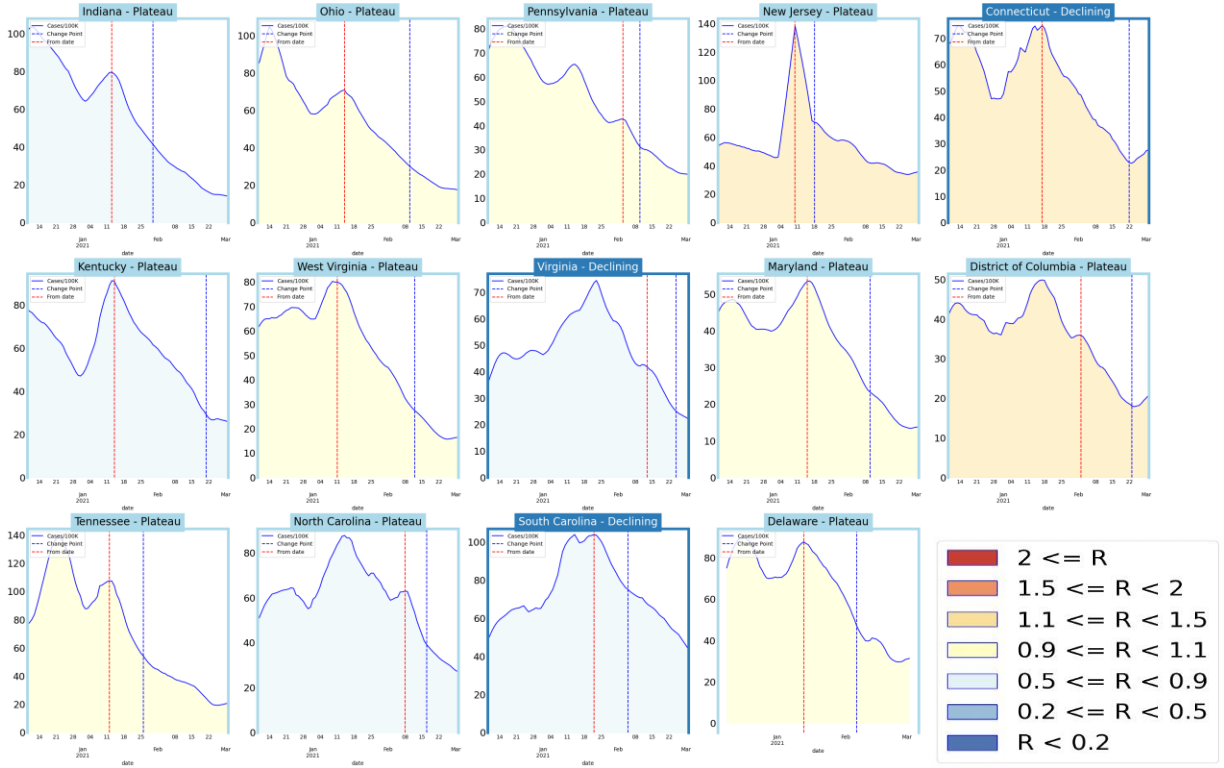
Other State Comparisons

Trajectories of States



- All states are declining (11) or plateaued (43)
- Re ticks up in many states indicating possible return to growth
- Rates remain elevated, as more declines are level off

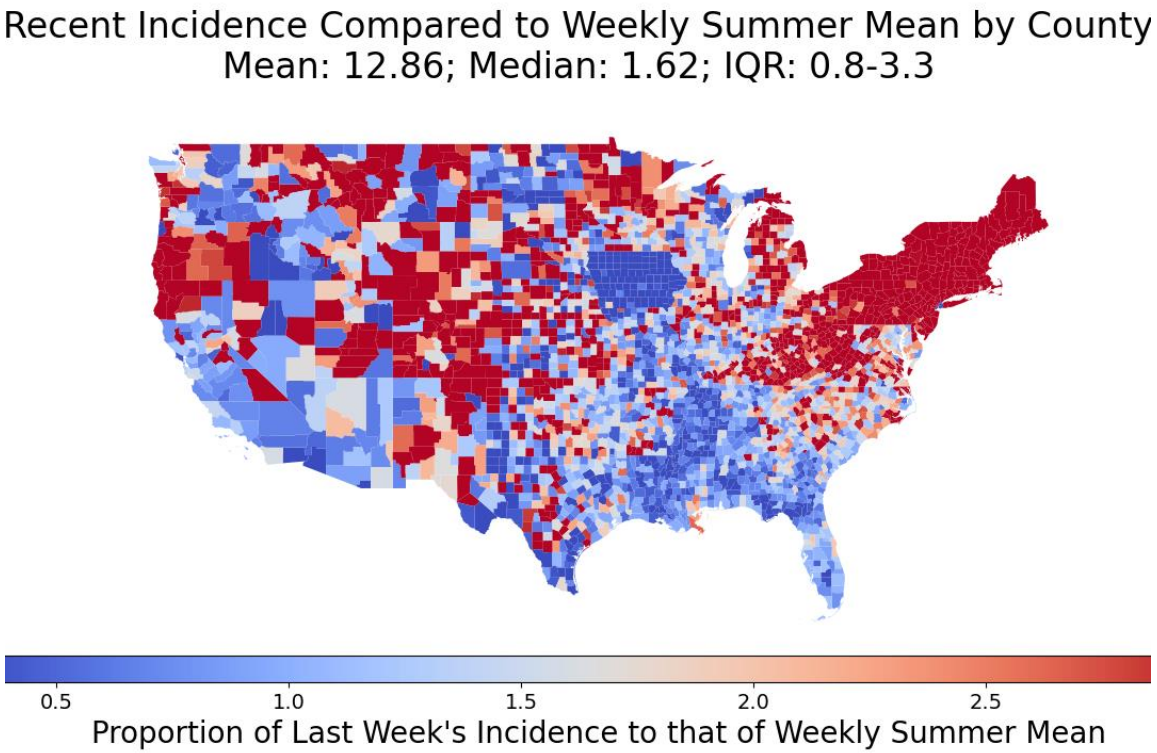
Virginia and her neighbors



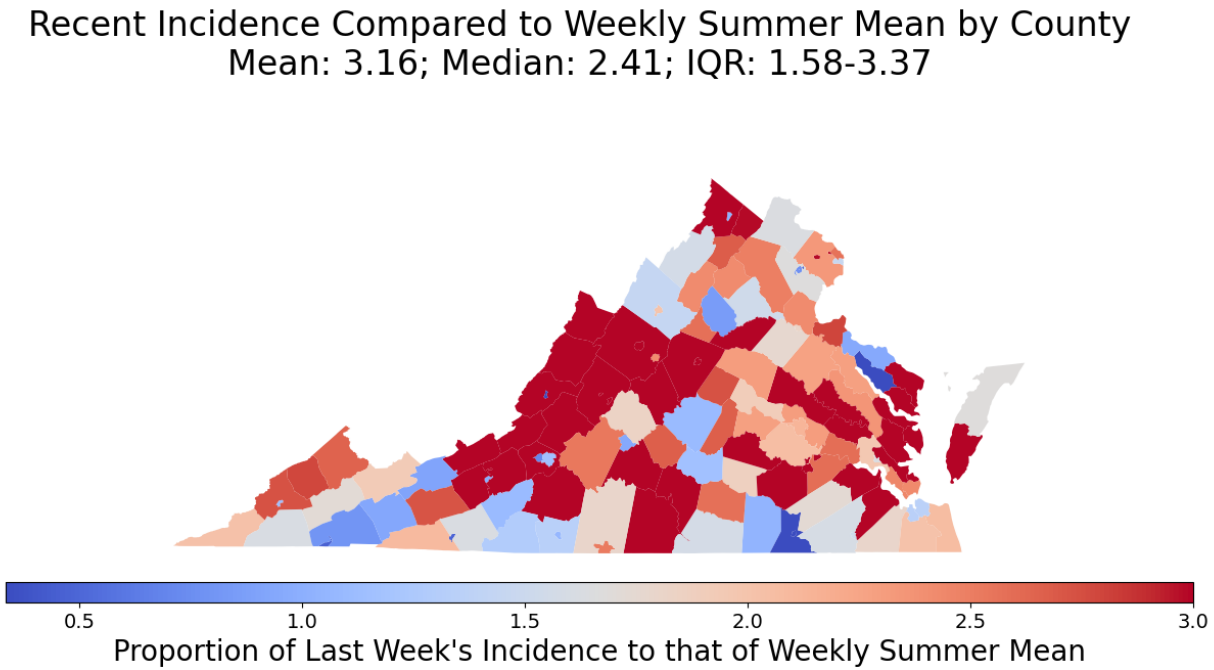
- VA remains in decline but many of her neighbors are shifting from decline to plateau, with some signs of a return to growth
- Rates remain elevated as rates of decline slow

Current Week vs. Summer Mean (June-Aug 2020)

Still some way to go to return to rates experienced during the summer of 2020 (June through August)



- 68% of US counties are above the summer mean case rate compared to 73% last week



- 88% of VA counties are above the average rate for the summer compared to 92% last week

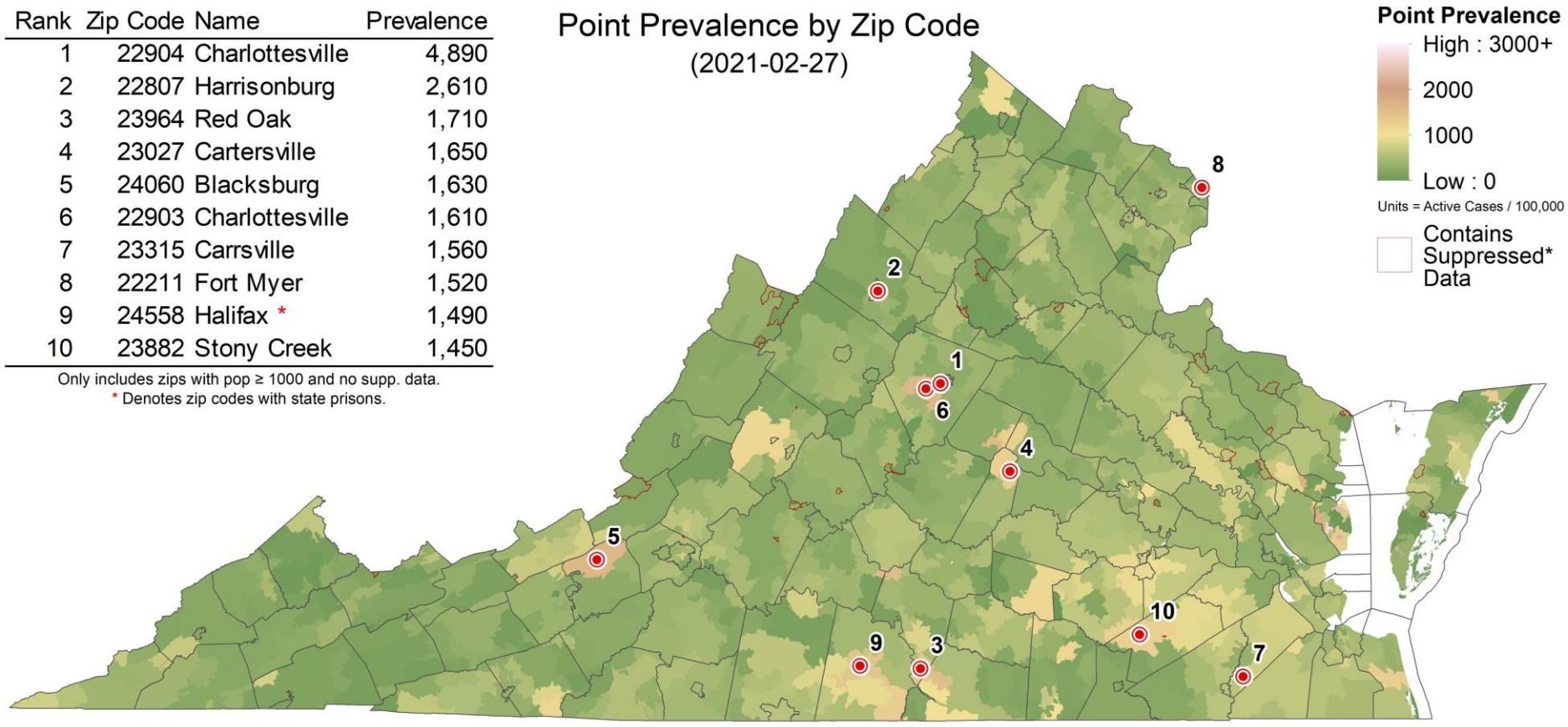
Zip code level weekly Case Rate (per 100K)

Case Rates in the last week by zip code

- Universities still dominate the top 10 list
- Concentrations of high rates scattered across the Commonwealth
- Some counts are low and suppressed to protect anonymity, those are shown in white

Rank	Zip Code	Name	Prevalence
1	22904	Charlottesville	4,890
2	22807	Harrisonburg	2,610
3	23964	Red Oak	1,710
4	23027	Cartersville	1,650
5	24060	Blacksburg	1,630
6	22903	Charlottesville	1,610
7	23315	Carrsville	1,560
8	22211	Fort Myer	1,520
9	24558	Halifax *	1,490
10	23882	Stony Creek	1,450

Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



Based on spatial empirical Bayes smoothed point prevelence for week ending 2021-02-27

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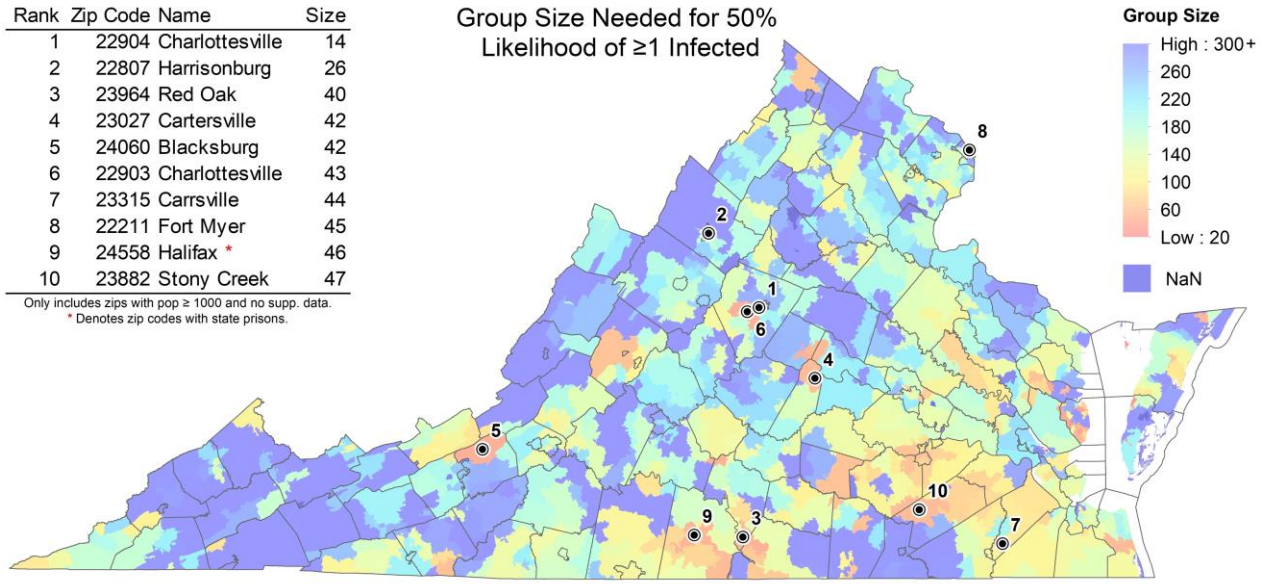
Risk of Exposure by Group Size

Case Prevalence in the last week by zip code used to calculate risk of encountering someone infected in a gathering of randomly selected people (group size 25)

- Assumes 3 undetected infections per confirmed case (ascertainment rate from recent seroprevalence survey)
- On left, minimum size of a group with a 50% chance an individual is infected by zip code (eg in a group of 14 in Charlottesville, there is a 50% chance someone will be infected)
- Some zip codes have high likelihood of exposure even in groups of 25

Rank	Zip Code	Name	Size
1	22904	Charlottesville	14
2	22807	Harrisonburg	26
3	23964	Red Oak	40
4	23027	Cartersville	42
5	24060	Blacksburg	42
6	22903	Charlottesville	43
7	23315	Carrsville	44
8	22211	Fort Myer	45
9	24558	Halifax *	46
10	23882	Stony Creek	47

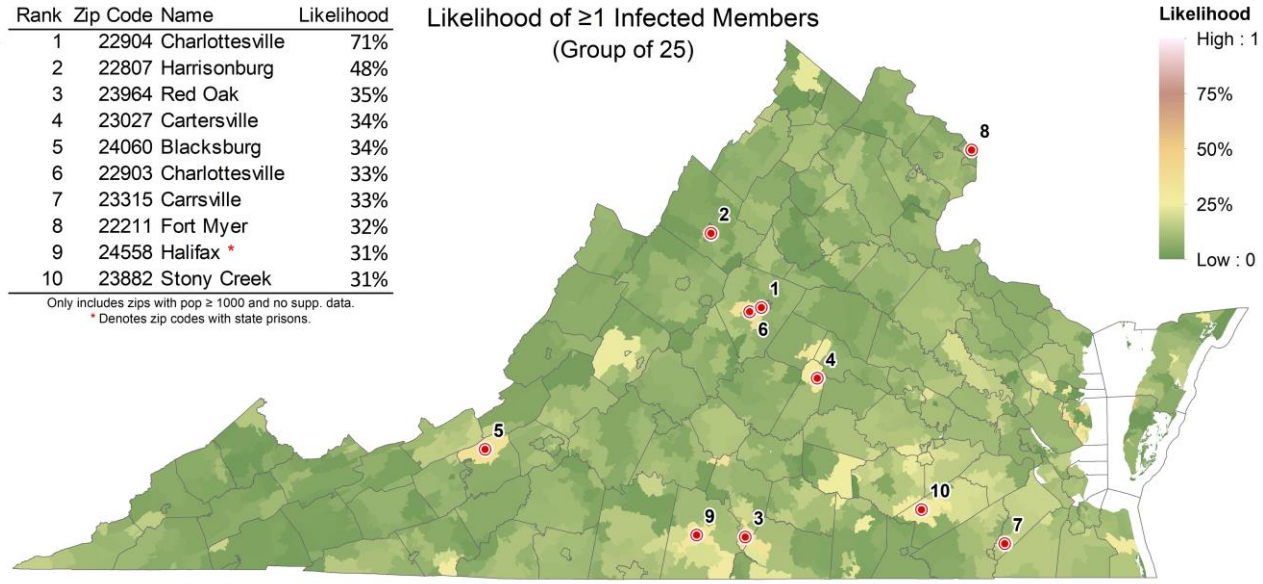
Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



Based on spatial empirical Bayes smoothed point prevelence for week ending 2021-02-27

Rank	Zip Code	Name	Likelihood
1	22904	Charlottesville	71%
2	22807	Harrisonburg	48%
3	23964	Red Oak	35%
4	23027	Cartersville	34%
5	24060	Blacksburg	34%
6	22903	Charlottesville	33%
7	23315	Carrsville	33%
8	22211	Fort Myer	32%
9	24558	Halifax *	31%
10	23882	Stony Creek	31%

Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.



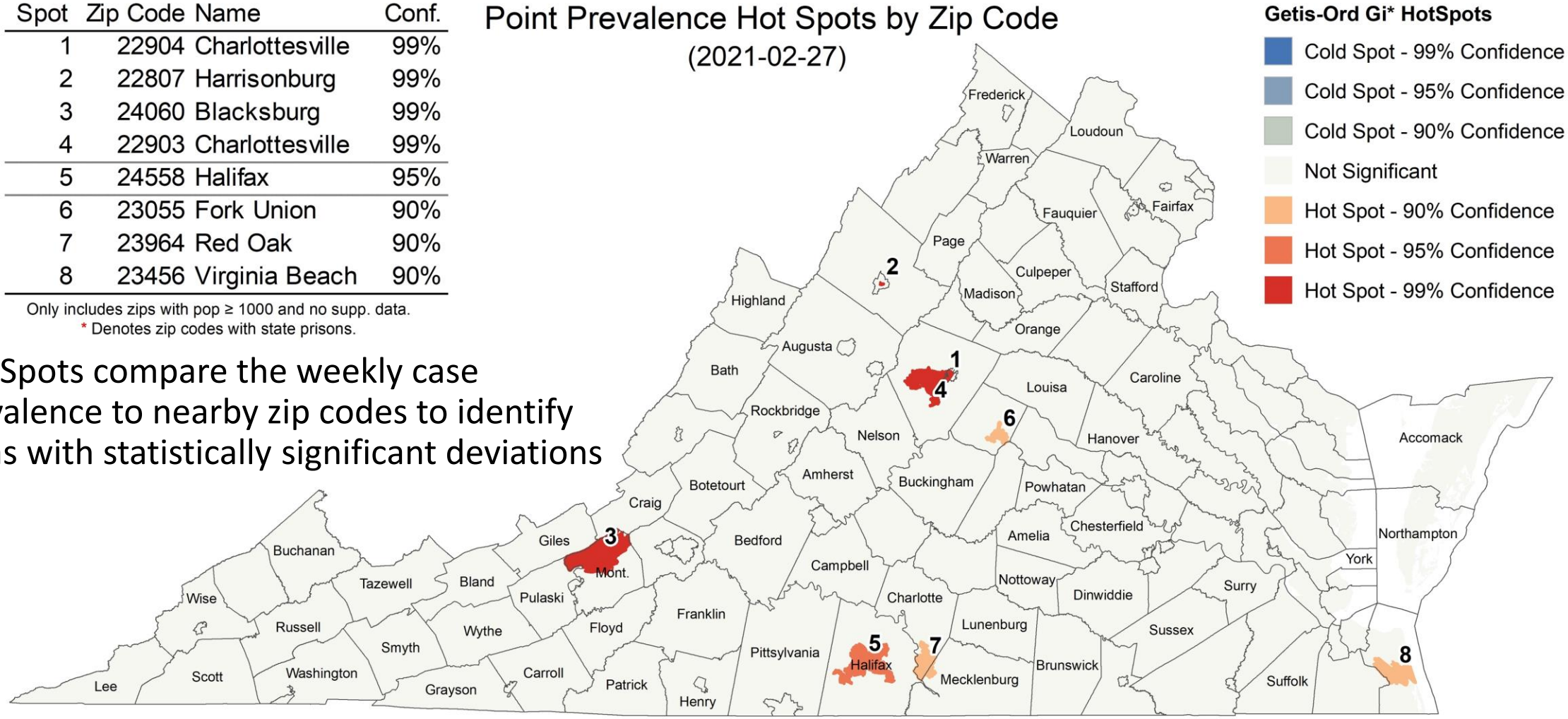
Based on spatial empirical Bayes smoothed point prevelence for week ending 2021-02-27

Current Spatial Hot Spots

Spot	Zip Code	Name	Conf.
1	22904	Charlottesville	99%
2	22807	Harrisonburg	99%
3	24060	Blacksburg	99%
4	22903	Charlottesville	99%
5	24558	Halifax	95%
6	23055	Fork Union	90%
7	23964	Red Oak	90%
8	23456	Virginia Beach	90%

Only includes zips with pop ≥ 1000 and no supp. data.
* Denotes zip codes with state prisons.

Hot Spots compare the weekly case prevalence to nearby zip codes to identify areas with statistically significant deviations



Based on global empirical Bayes smoothed point prevelence for week ending 2021-02-27

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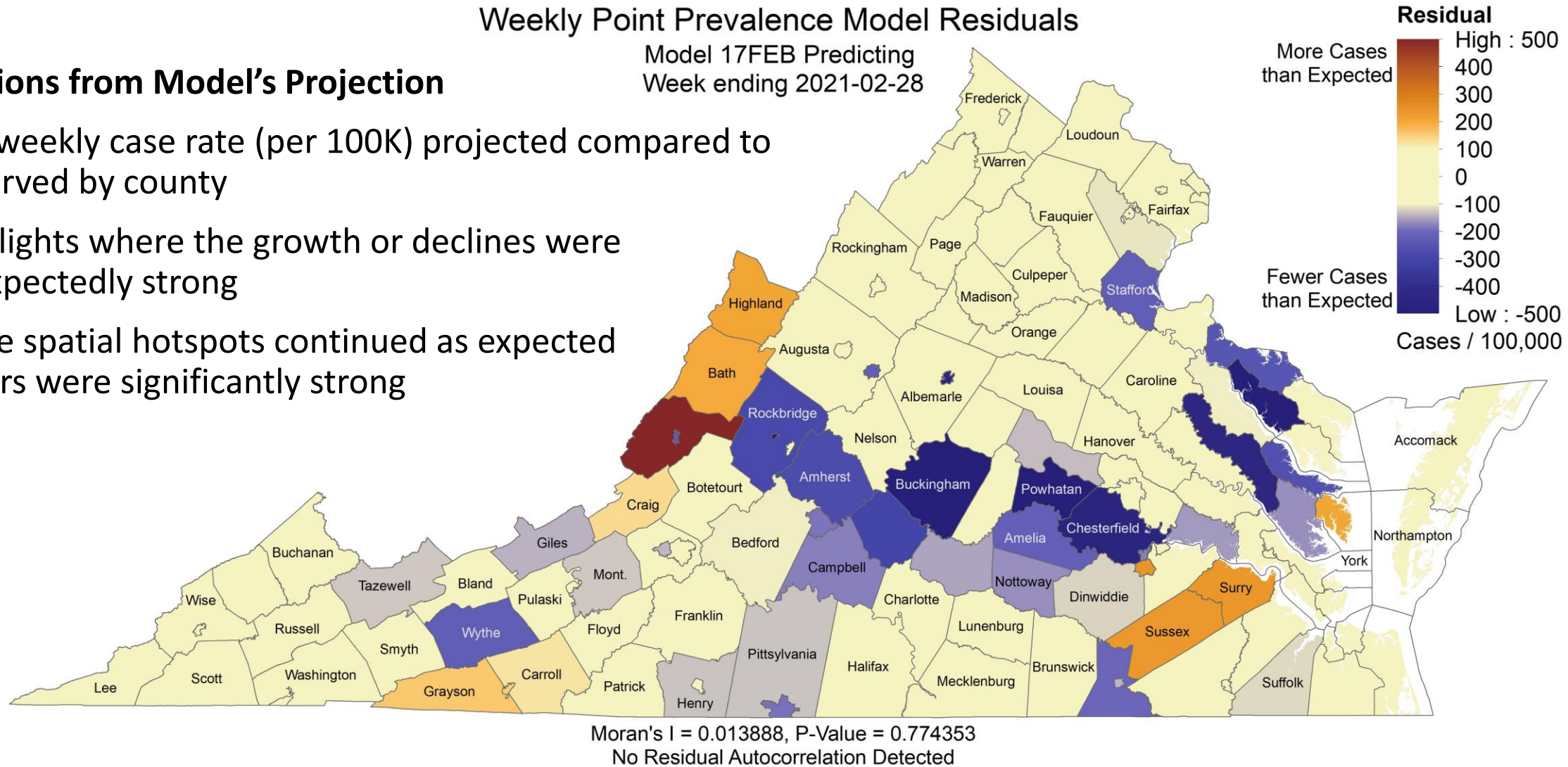
Current Spatial Hot Spots

Deviations from Model's Projection

- The weekly case rate (per 100K) projected compared to observed by county
- Highlights where the growth or declines were unexpectedly strong
- Some spatial hotspots continued as expected others were significantly strong



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Model Update – Adaptive Fitting

Adaptive Fitting Approach

Each county fit precisely, with recent trends used for future projection

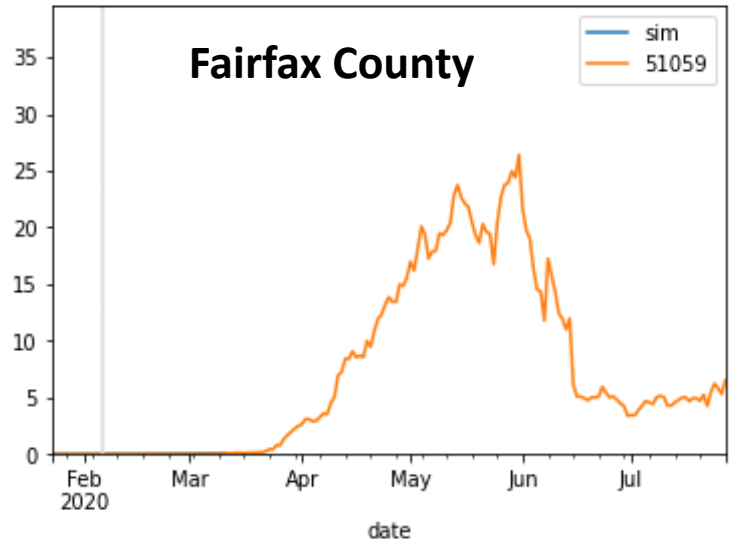
- Allows history to be precisely captured, and used to guide bounds on projections

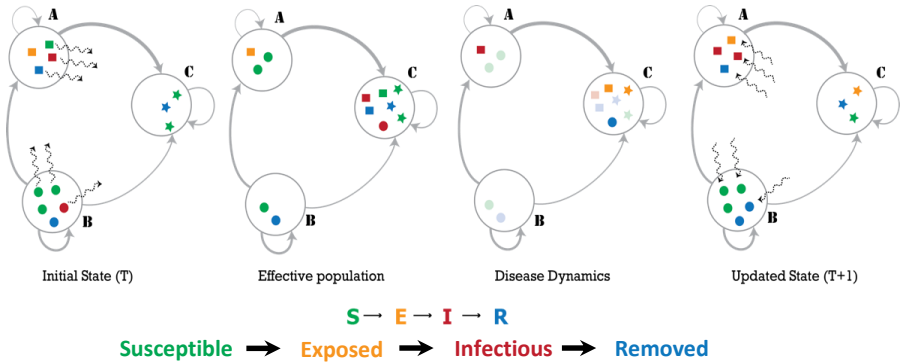
Model: An alternative use of the same meta-population model, PatchSim

- Allows for future "what-if" Scenarios to be layered on top of calibrated model
- Eliminates connectivity between patches, to allow calibration to capture the increasingly unsynchronized epidemic

External Seeding: Steady low-level importation

- Widespread pandemic eliminates sensitivity to initial conditions
- Uses steady 1 case per 10M population per day external seeding





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Using Ensemble Model to Guide Projections

Ensemble methodology that combines the Adaptive with machine learning and statistical models such as:

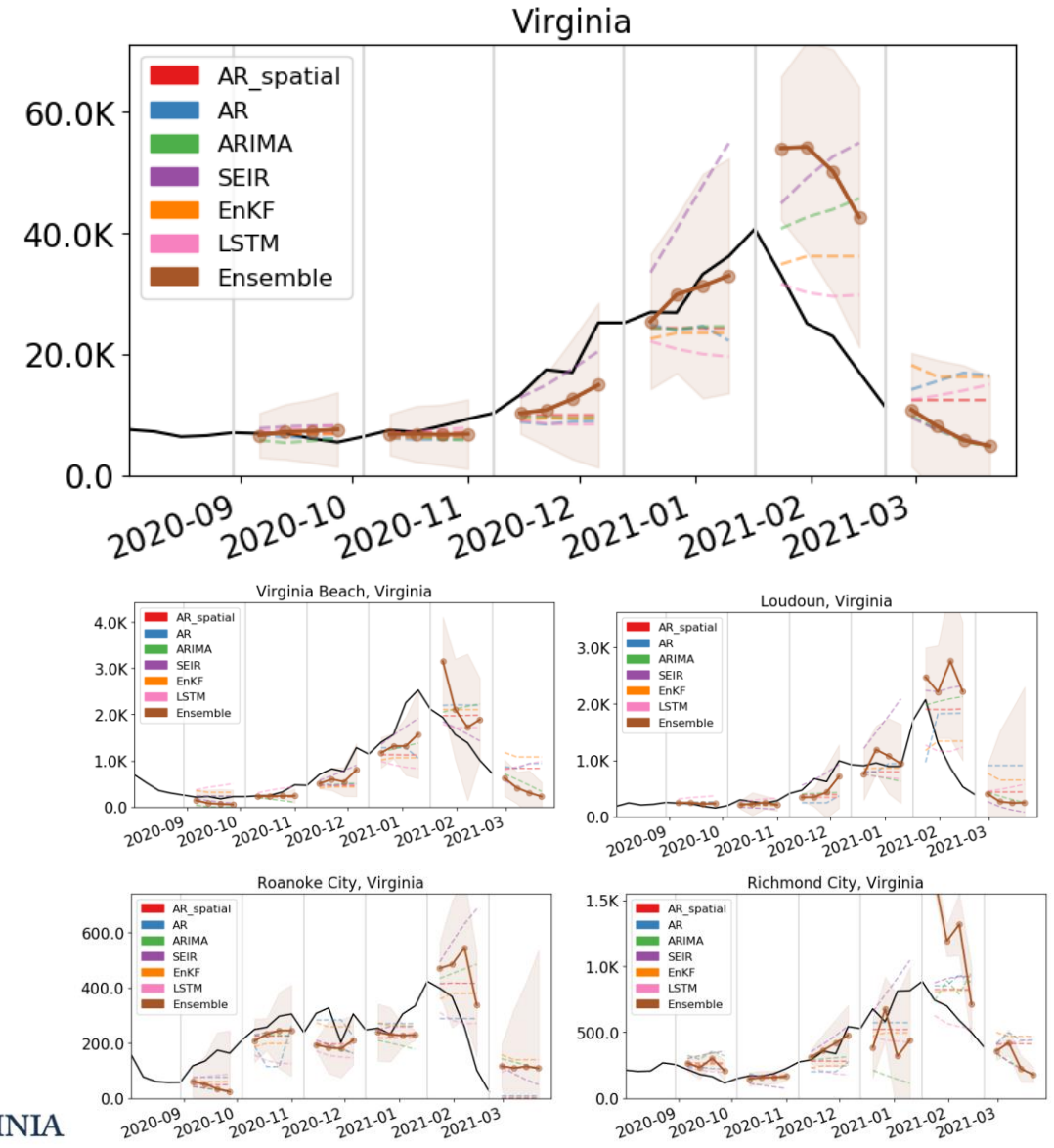
- Autoregressive (AR, ARIMA)
- Neural networks (LSTM)
- Kalman filtering (EnKF)

<u>Weekly forecasts</u> done at county level.

Models chosen because of their track record in disease forecasting and to increase diversity and robustness.

Ensemble forecast provides additional 'surveillance' for making scenario-based projections.

Also submitted to CDC Forecast Hub.



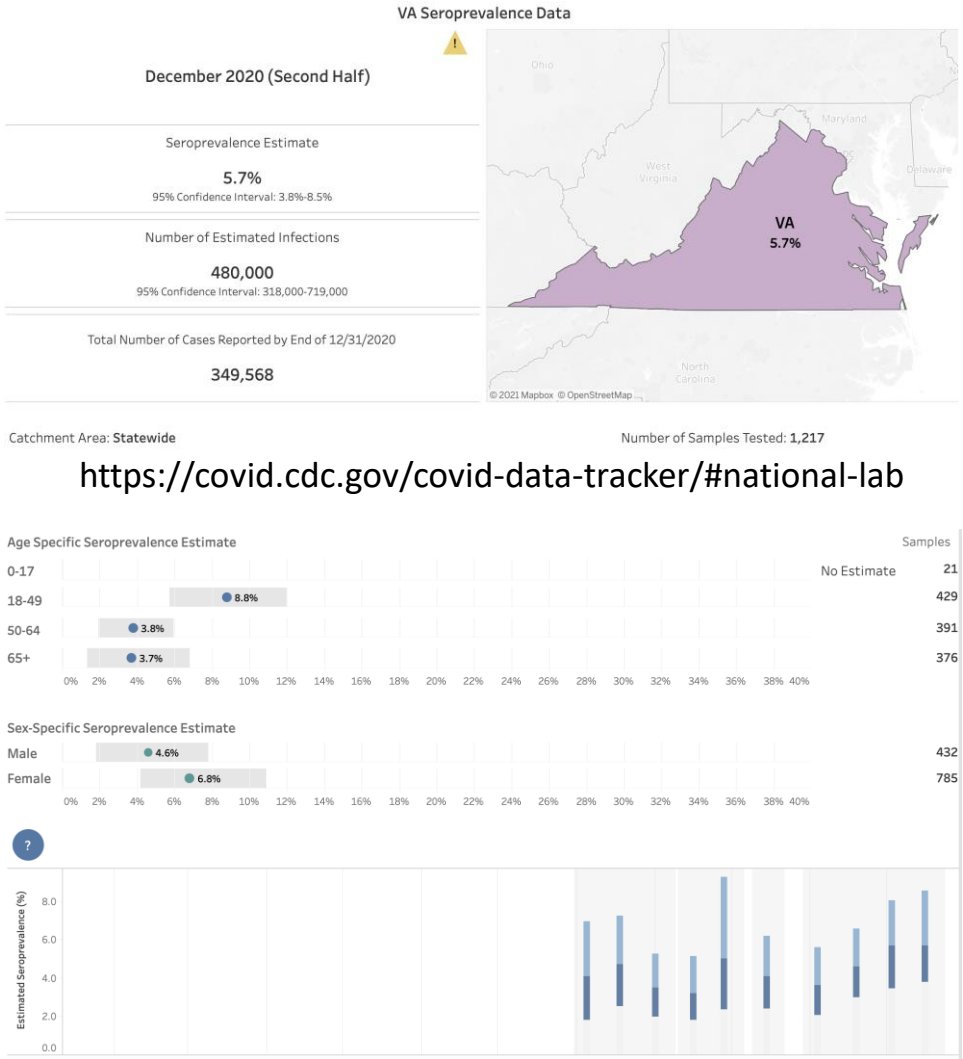
Seroprevalence updates to model design

Several seroprevalence studies provide better picture of how many actual infections have occurred

- CDC Nationwide Commercial Laboratory Seroprevalence Survey estimated 5.7% [3.8% – 8.5%] seroprevalence as of Dec 10th – 23rd from 4.6% a month earlier

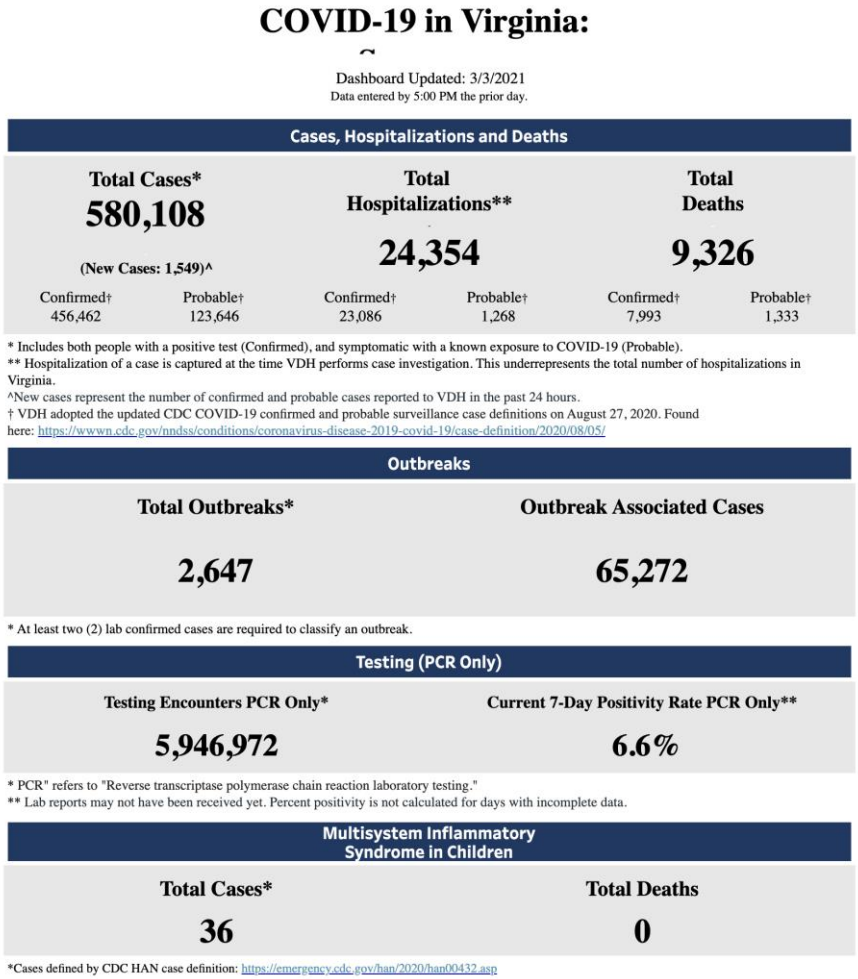
These findings are equivalent to an ascertainment ratio of ~2x in the future, with bounds of (1.3x to 3x)

- Thus for 2x there are 2 total infections in the population for every confirmed case recently
- This measure now fully tracks the estimated ascertainment over time
- Uncertainty design has been shifted to these bounds (previously higher ascertainments as was consistent earlier in the pandemic were being used)



Calibration Approach

- **Data:**
  - County level case counts by date of onset (from VDH)
  - Confirmed cases for model fitting
- **Calibration:** fit model to observed data and ensemble's forecast
  - Tune transmissibility across ranges of:
    - Duration of incubation (5-9 days), infectiousness (3-7 days)
    - Undocumented case rate (1x to 7x) guided by seroprevalence studies
    - Detection delay: exposure to confirmation (4-12 days)
  - Approach captures uncertainty, but allows model to precisely track the full trajectory of the outbreak
- **Project:** future cases and outcomes generated using the collection of fit models run into the future
  - **Mean trend from last 7 days of observed cases and first week of ensemble's forecast used**
  - Outliers removed based on variances in the previous 3 weeks
  - 2 week interpolation to smooth transitions in rapidly changing trajectories



COVID-19 in Virginia:

Dashboard Updated: 3/3/2021
Data entered by 5:00 PM the prior day.

Cases, Hospitalizations and Deaths

Total Cases*		Total Hospitalizations**		Total Deaths	
580,108		24,354		9,326	
(New Cases: 1,549)^					
Confirmed†	Probable†	Confirmed†	Probable†	Confirmed†	Probable†
456,462	123,646	23,086	1,268	7,993	1,333

* Includes both people with a positive test (Confirmed), and symptomatic with a known exposure to COVID-19 (Probable).
** Hospitalization of a case is captured at the time VDH performs case investigation. This underrepresents the total number of hospitalizations in Virginia.
^New cases represent the number of confirmed and probable cases reported to VDH in the past 24 hours.
† VDH adopted the updated CDC COVID-19 confirmed and probable surveillance case definitions on August 27, 2020. Found here: https://wwwn.cdc.gov/nndss/conditions/coronavirus-disease-2019-covid-19/case-definition/2020/08/05/

Outbreaks

Total Outbreaks*	Outbreak Associated Cases
2,647	65,272

* At least two (2) lab confirmed cases are required to classify an outbreak.

Testing (PCR Only)

Testing Encounters PCR Only*	Current 7-Day Positivity Rate PCR Only**
5,946,972	6.6%

* PCR" refers to "Reverse transcriptase polymerase chain reaction laboratory testing."
** Lab reports may not have been received yet. Percent positivity is not calculated for days with incomplete data.

Multisystem Inflammatory Syndrome in Children

Total Cases*	Total Deaths
36	0

*Cases defined by CDC HAN case definition: https://emergency.cdc.gov/han/2020/han00432.asp

Accessed 9:00am March 3, 2021

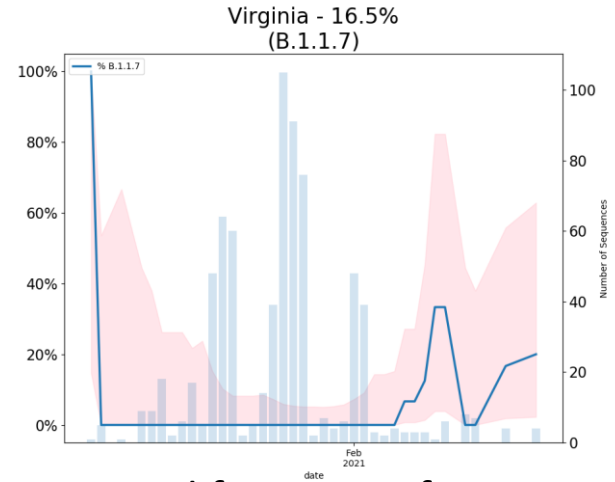
https://www.vdh.virginia.gov/coronavirus/

Scenarios – Seasonal Effects

- Variety of factors continue to drive transmission rates
  - Seasonal impact of weather patterns, travel and gatherings, fatigue and premature relaxation of infection control practices.
- Plausible levels of transmission can be bounded by past experience
  - Assess transmission levels at the county level since May 2020
  - Use the highest and lowest levels experienced (excluding outliers) as plausible bounds for levels of control achievable
  - Transition from current levels of projection to the new levels over 2 months
- New planning Scenarios:
  - **Best of the Past**: Lowest level of transmission (10^{th} percentile)
  - **Fatigued Control**: Highest level of transmission (95^{th} percentile) increased by additional 5%

Scenarios – Novel Variants

- Several novel variants of SARS-CoV2 are being tracked
  - Some are more transmissible, some may escape immunity from previous natural infection and/or vaccination, others may be more severe
- New Variant B.1.1.7 is best understood and is in Virginia
  - **Transmission increase**: Several different studies have estimated the increase in transmission to be 30-55%, we use 40% increase from the current baseline projection
  - **Emergence timing:** Gradually assumes predominance over the next 6 weeks, reaching 50% frequency in late March as estimated in a recent MMWR report from CDC and refined by Andersen et al.
- Variant planning Scenario:
  - **VariantB117**: Current projected transmissibility increases gradually over 4 months to level 40% more transmissible

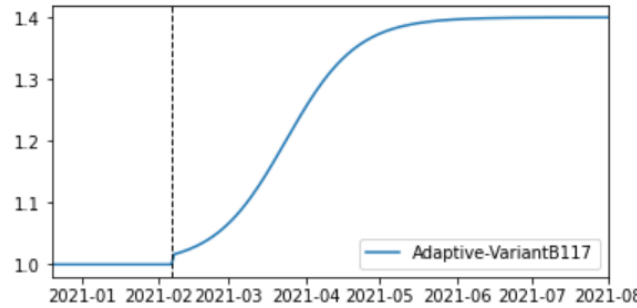


Estimated frequency from public genome repository with added analysis: 16.5%

outbreak.info

GISAID

Outbreak Info



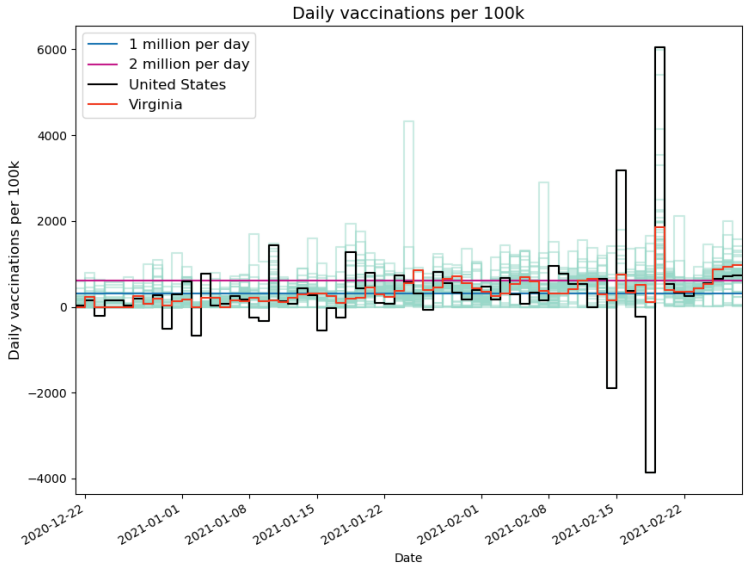
Current frequency used in model: 16.7%

Scenarios – Vaccines

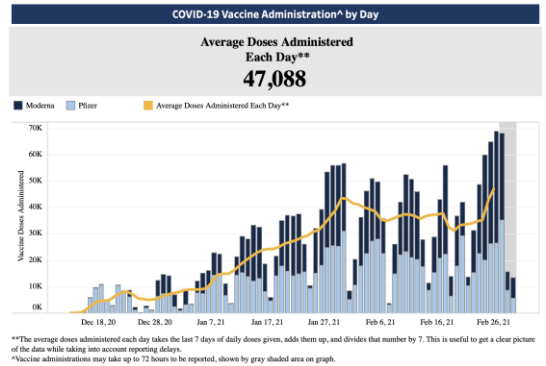
- Vaccination has started, and efforts are underway to increase its pace
  - Exact achievable rollouts and level of coverage are unknown, though coming into focus
- Vaccine efficacy varies over course of vaccine
  - FDA EUAs show 50% efficacy achieved 2 weeks after 1st dose, and 95% 2 weeks after 2nd dose
  - Assuming 3.5 week (average of Pfizer and Moderna) gap between doses
- Vaccine hesitancy poses a future problem
  - Currently demand far outpaces supply so we assume all courses will be administered until we reach the hesitancy threshold, for 50% this is several months in the future.

Current rollouts and scenarios inspired by MIDAS Network COVID-19 Scenario Hub: https://github.com/midas-network/covid19-scenario-modeling-hub

VA Vaccination Rates



Lines represent 1M & 2M total doses administered a day (rate of 303/100K & 606/100K)

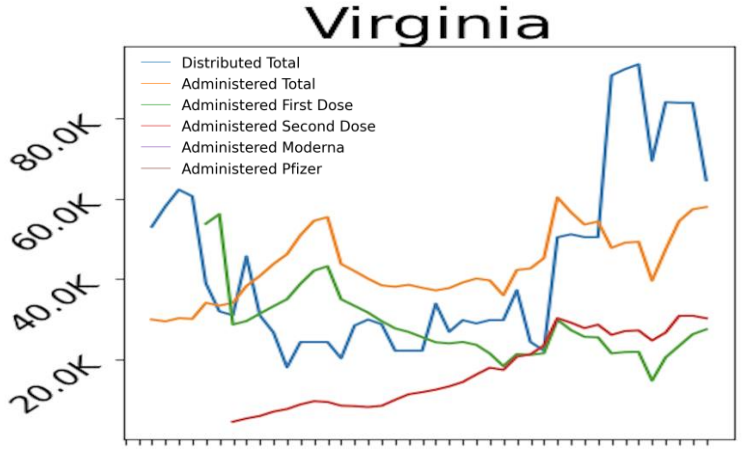


Accessed 8:30pm March 2, 2021
https://www.vdh.virginia.gov/coronavirus/covid-19-vaccine-summary/

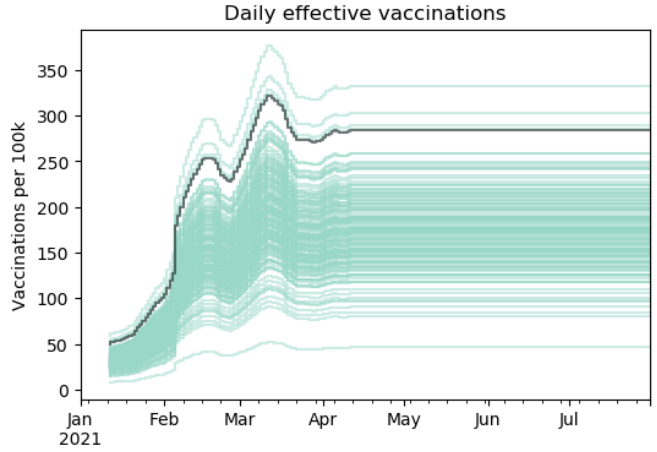
Scenarios – Vaccines

- Administration schedule uses actual administration and expected for the future
  - Use history of state-specific doses administered as captured by Bloomberg (up to Jan 19th) and CDC (Jan 20th and on)
  - Vaccination rate specific to each county (as obtained through VDH dashboard) vax data in data package
  - Future courses based on sustaining daily average of most recent week
    - **Rate**: 299 **FIRST DOSES** per 100K per day or a total of ~25K 1st doses per day, which is up from last week's levels
    - **Total Amount**: This pace leads to eventually reaching 50K administered a day, implying 25K fully vaccinated a day
    - **Location**: Per capita distribution across all counties

Fluctuations in dosages over time



Modeled Vaccine Induced Immunity



All VA counties, state in black

Current rollouts and scenarios inspired by MIDAS Network COVID-19 Scenario Hub: https://github.com/midas-network/covid19-scenario-modeling-hub

Scenarios – Seasonal Effects and Vaccines

Three scenarios combine these seasonal effects and use the updated vaccine schedule

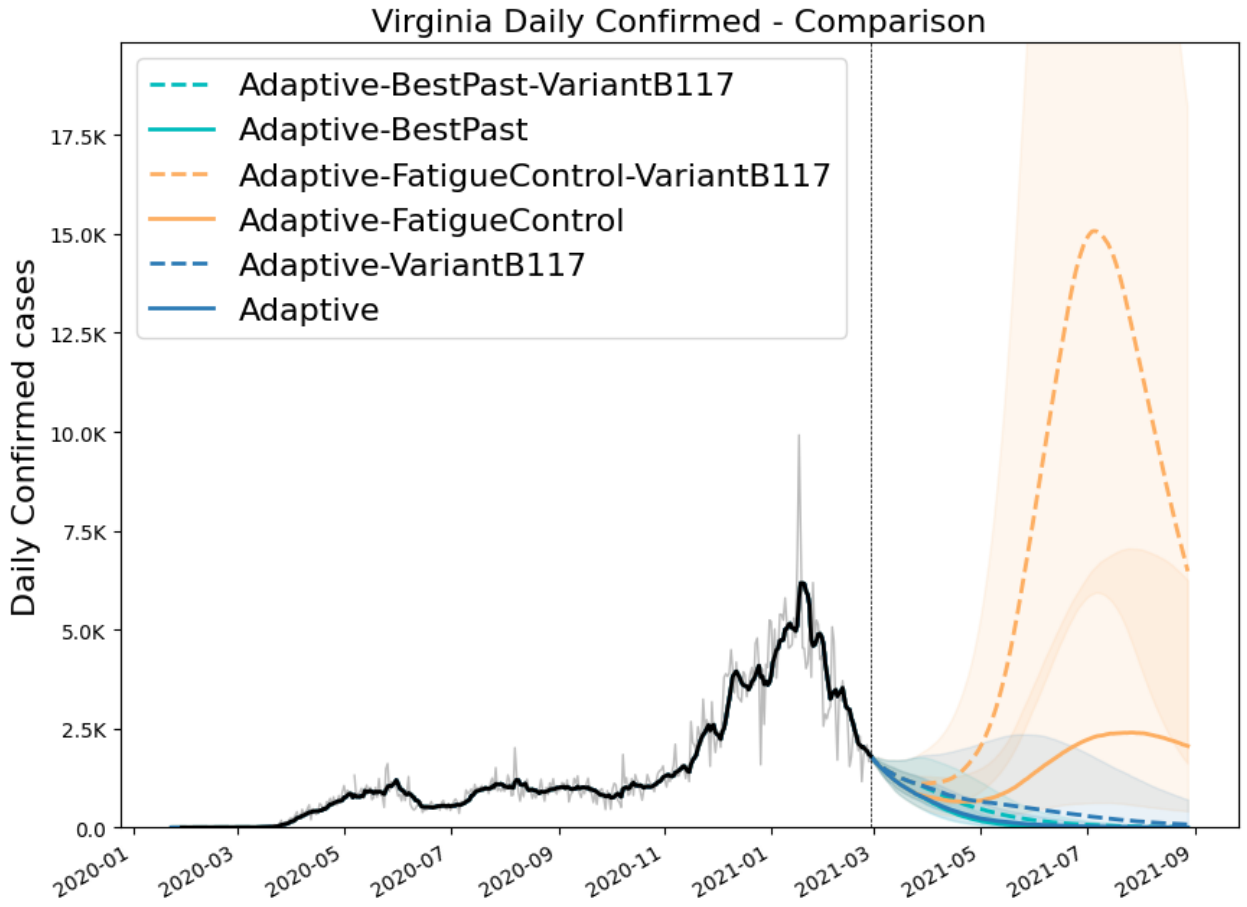
- **Adaptive**: No seasonal effects from base projection
  - If things continue as they are
- **Adaptive-FatigueControl**: Fatigued control seasonal effects
  - If we revert to slightly worst transmission experienced in last 6 months
- **Adaptive-BestPast**: Best of the past control seasonal effects
  - If we revert to best control experienced in last 6 months
- **Adaptive-VariantB117**: Boosting of transmissibility from the emergence of B.1.1.7
  - If new variants begin to predominate and boost transmission, this assumes current seasonal affects remain the same (eg like Adaptive)
- **Adaptive-FatigueControl-VariantB117:** Fatigued control and txm boost from B.1.1.7
- **Adaptive-BestPast-VariantB117:** Best of the past control vs. txm boost from B.1.1.7

Counterfactuals with no vaccine ("NoVax") are provided for comparison purposes

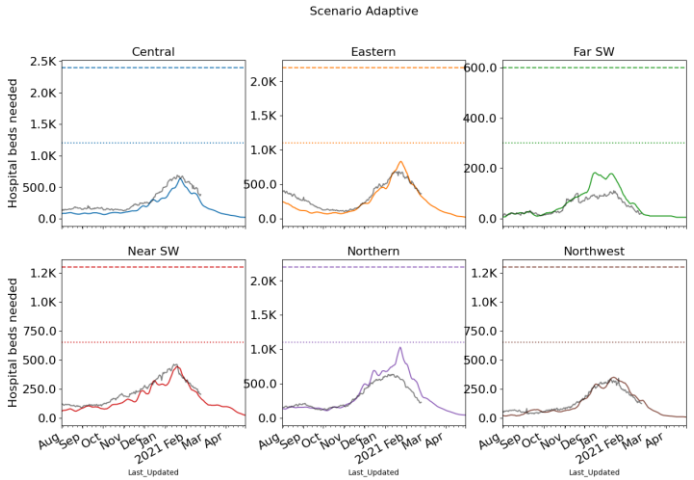
Model Results

Outcome Projections

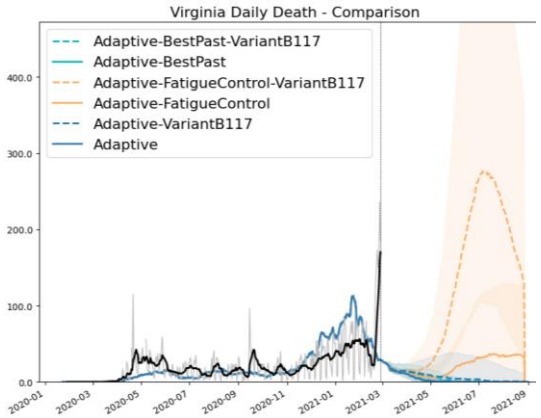
Confirmed cases



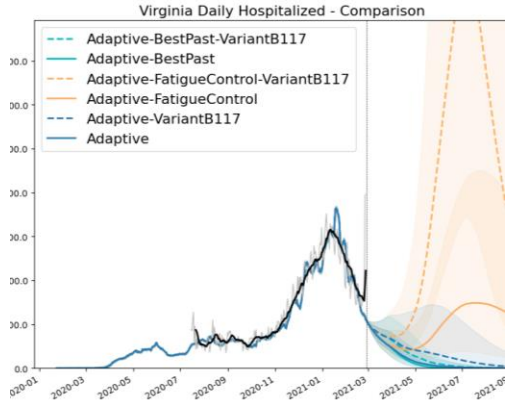
Estimated Hospital Occupancy



Daily Deaths



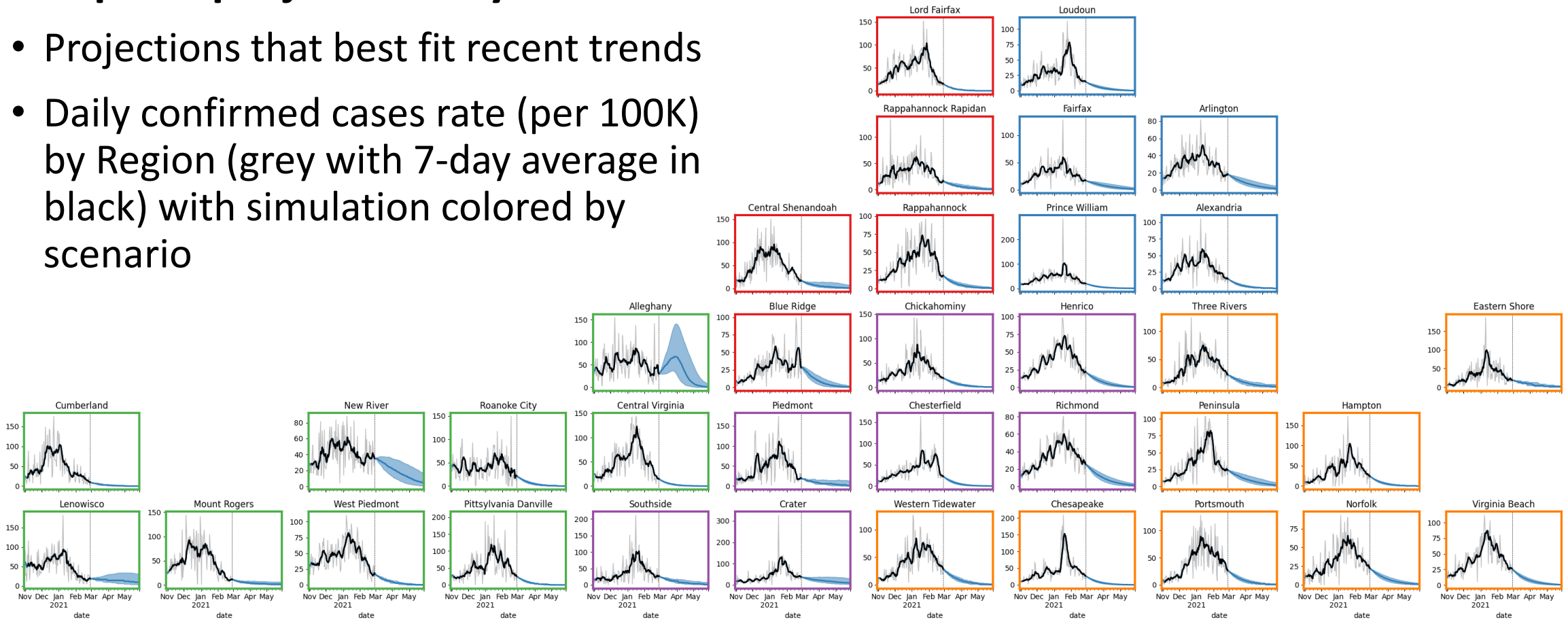
Daily Hospitalized



District Level Projections: Adaptive

Adaptive projections by District

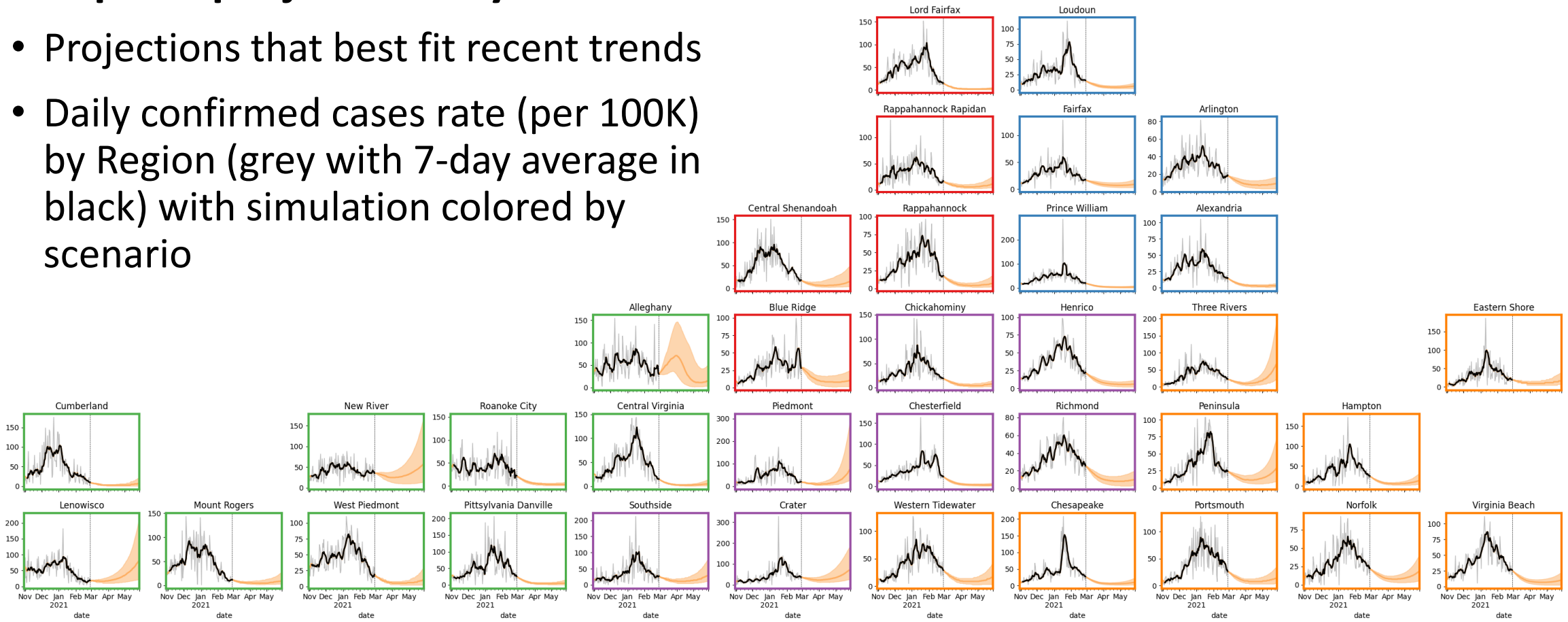
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl

Adaptive projections by District

- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



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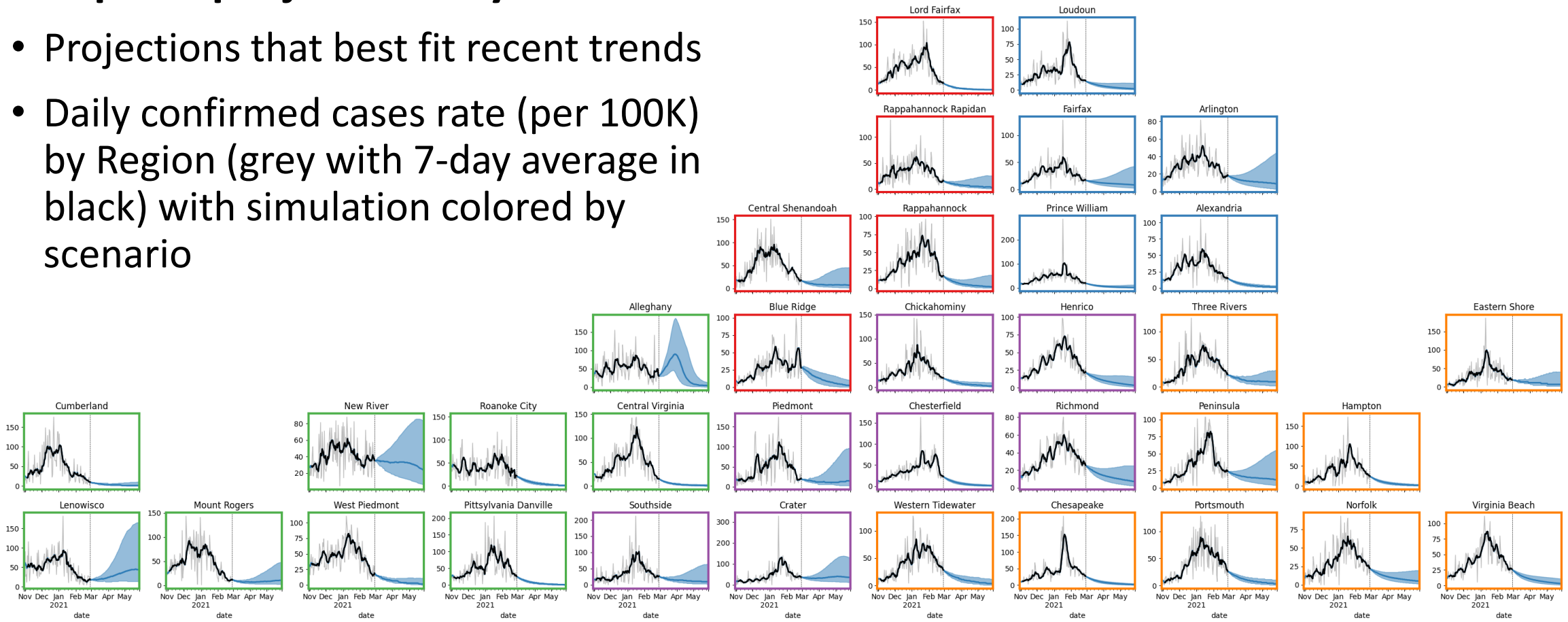
District Level Projections: Adaptive-VariantB117

Adaptive projections by District

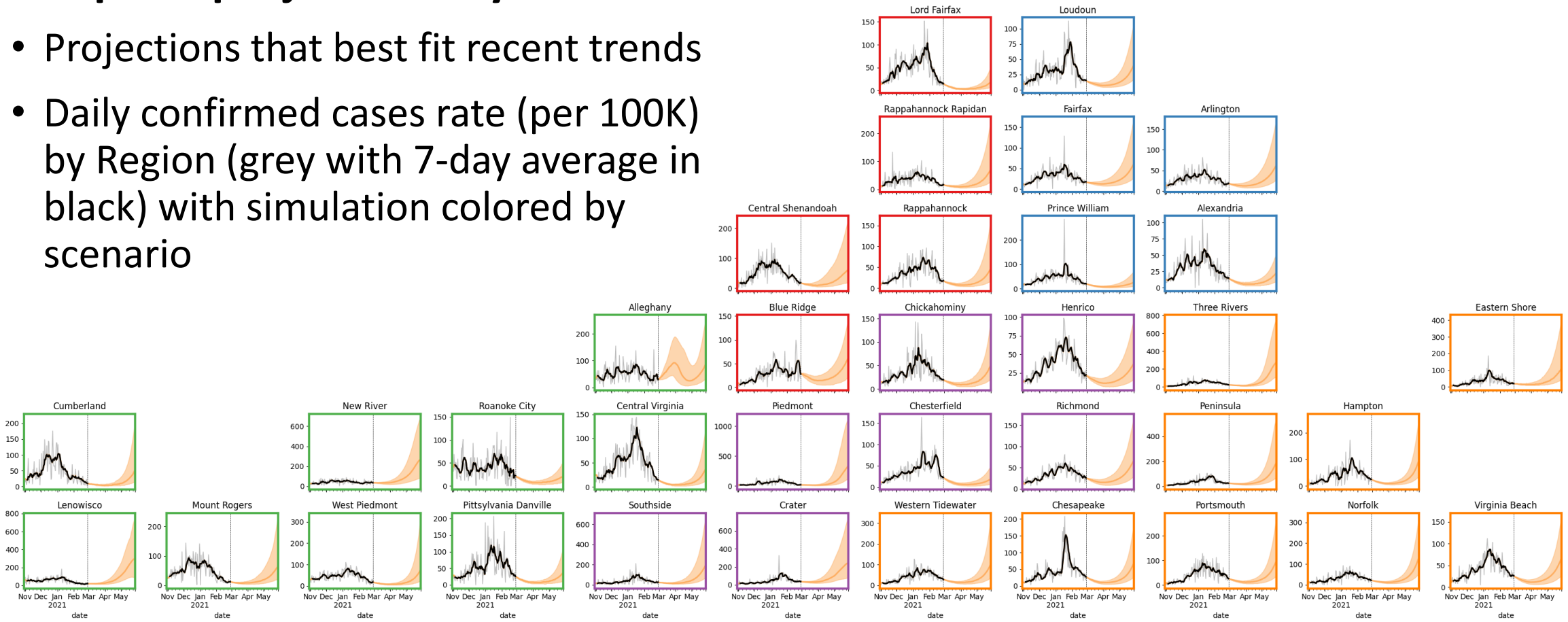
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario



District Level Projections: Adaptive-FatigueControl-VariantB117

Adaptive projections by District

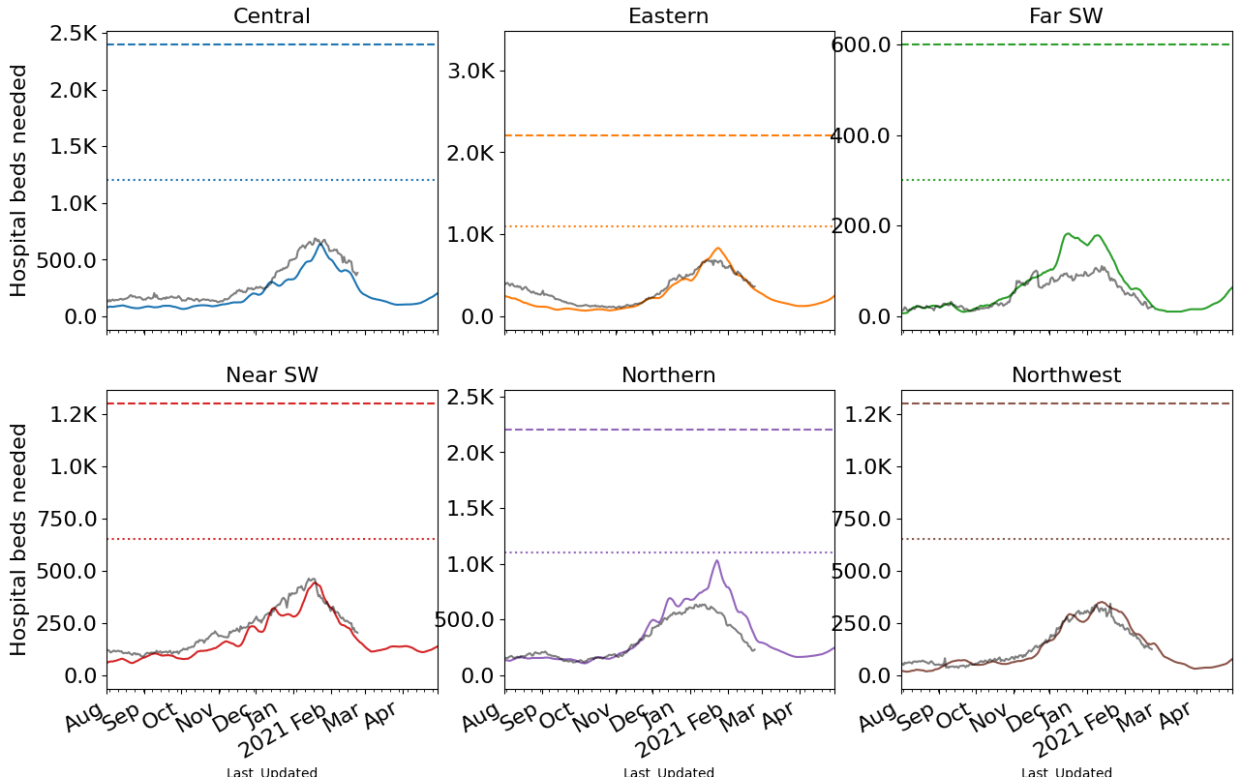
- Projections that best fit recent trends
- Daily confirmed cases rate (per 100K) by Region (grey with 7-day average in black) with simulation colored by scenario

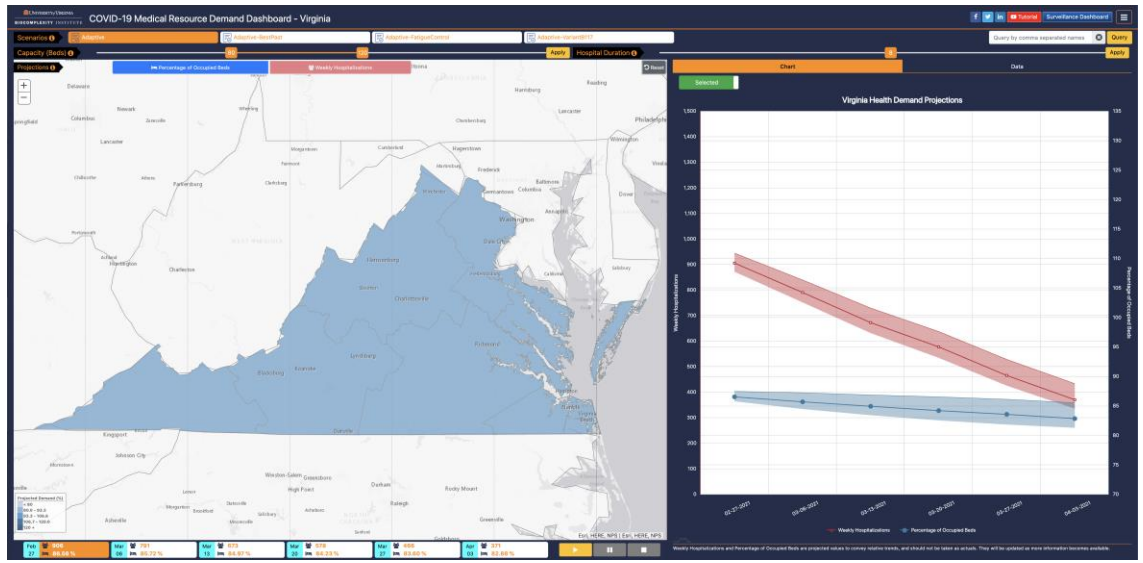


Hospital Demand and Bed Capacity by Region

Capacities* by Region – Adaptive-FatigueControl-VariantB117

COVID-19 capacity ranges from 80% (dots) to 120% (dash) of total beds





https://nssac.bii.virginia.edu/covid-19/vmrddash/

If Adaptive-FatigueControl-Variant scenario:

- Surge bed capacity is unlikely to be reached in coming 4 months

* Assumes average length of stay of 8 days

Weekly Cases and Hospitalizations

Weekly confirmed cases

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
2/28/21	13,381	13,380	13,380	13,380	13,380
3/7/21	10,897	10,898	10,904	11,074	11,079
3/14/21	8,856	8,868	8,878	9,642	9,642
3/21/21	7,256	7,278	7,292	8,568	8,559
3/28/21	5,989	6,073	5,990	7,779	7,870
4/4/21	4,935	5,433	4,824	7,069	7,809
4/11/21	3,921	5,014	3,669	6,300	8,073
4/18/21	3,052	4,680	2,695	5,566	8,824
4/25/21	2,352	4,571	1,906	5,050	10,496
5/2/21	1,783	4,683	1,308	4,672	13,295
5/9/21	1,364	5,108	902	4,400	17,720
5/16/21	1,078	5,856	603	4,126	24,495

Weekly Hospitalizations

Week Ending	Adaptive	Adaptive-Fatigued Control	Adaptive-BestPast	Adaptive-VariantB117	Adaptive-Fatigued Control -VariantB117
2/28/21	919	919	919	919	919
3/7/21	719	719	719	730	730
3/14/21	597	599	599	646	646
3/21/21	471	472	473	582	582
3/28/21	373	377	373	503	508
4/4/21	314	340	307	453	510
4/11/21	244	314	223	401	526
4/18/21	161	290	140	356	583
4/25/21	125	282	102	319	717
5/2/21	93	293	67	296	950
5/9/21	77	323	47	266	1,254
5/16/21	54	369	26	258	1,734

Key Takeaways

Projecting future cases precisely is impossible and unnecessary.
Even without perfect projections, we can confidently draw conclusions:

- **Case rate growth in Virginia continues to decline with a few hotspots emerging**
- VA mean weekly incidence down to 19/100K from 23/100K, US levels decline (to 18 from 19 per 100K)
- Significant progress made in last month, however 88% of VA counties above mean rate of Summer 2020
- Projections continue to be down across Commonwealth
- Recent updates:
  - Adjustment to death outcome modeling to correct for delays in reporting, higher resolution hospital data incorporated for hospital calibration
  - Ascertainment rate adjusted to better capture total infections to date
  - Further updates to vaccination schedules, with fitting now including partially vaccinated population and future vaccinations based on current levels instead of goals
- The situation is changing rapidly. Models continue to be updated regularly.

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Venkatramanan, S., et al. "Optimizing spatial allocation of seasonal influenza vaccine under temporal constraints." *PLoS computational biology* 15.9 (2019): e1007111.

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Google. COVID-19 community mobility reports. https://www.google.com/covid19/mobility/

Biocomplexity page for data and other resources related to COVID-19: https://covid19.biocomplexity.virginia.edu/

Questions?

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Supplemental Slides

Date of Onset Reproductive Number

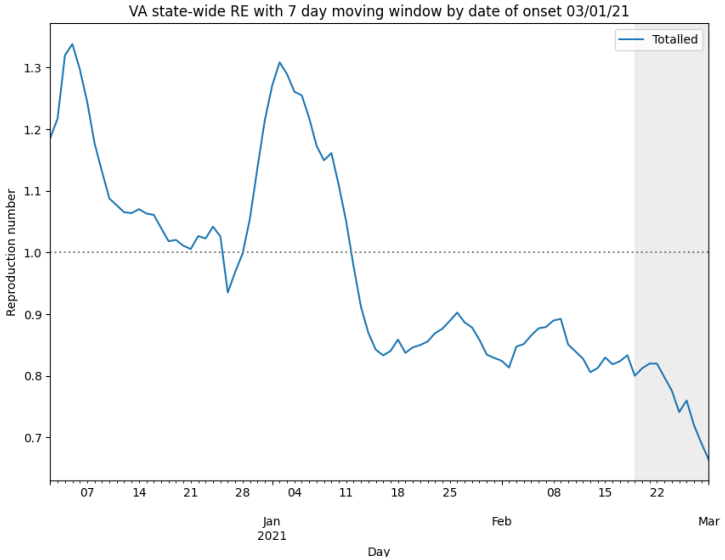
Feb 20th Estimates

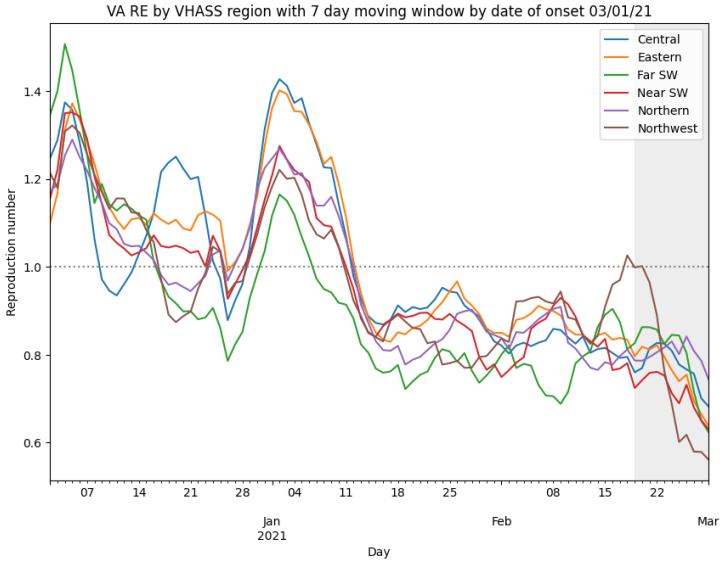
Region	Date of Onset R_e	Date Onset Diff Last Week
State-wide	0.812	0.011
Central	0.770	-0.058
Eastern	0.818	0.003
Far SW	0.863	0.125
Near SW	0.742	-0.057
Northern	0.786	0.016
Northwest	1.002	0.179

Methodology

- Wallinga-Teunis method (EpiEstim[1]) for cases by date of onset
- Serial interval: 6 days (2 day std dev)
- Recent estimates may be unstable due to backfill

1. Anne Cori, Neil M. Ferguson, Christophe Fraser, Simon Cauchemez. A New Framework and Software to Estimate Time-Varying Reproduction Numbers During Epidemics. American Journal of Epidemiology, Volume 178, Issue 9, 1 November 2013, Pages 1505–1512, https://doi.org/10.1093/aje/kwt133

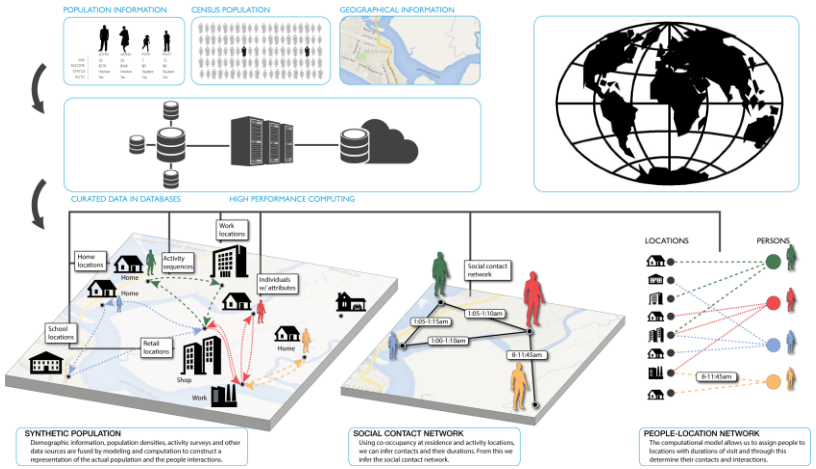




Agent-based Model (ABM)

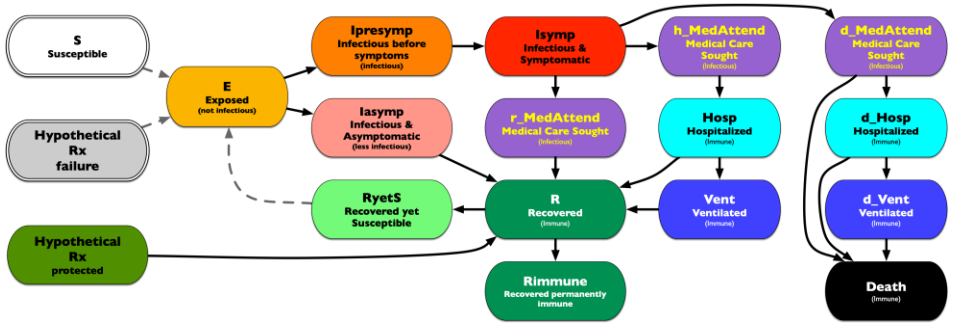
EpiHiper: Distributed network-based stochastic disease transmission simulations

- Assess the impact on transmission under different conditions
- Assess the impacts of contact tracing



Synthetic Population

- Census derived age and household structure
- Time-Use survey driven activities at appropriate locations



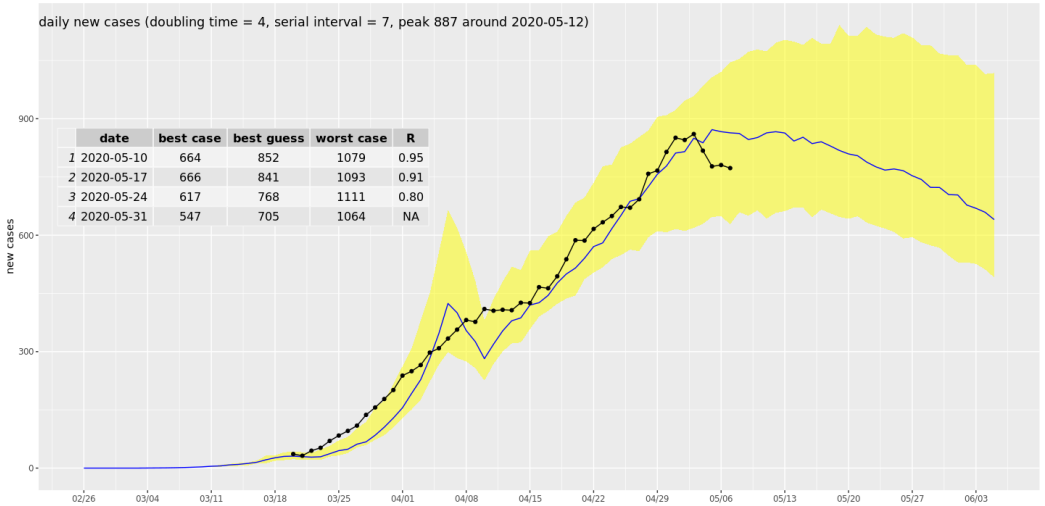
Detailed Disease Course of COVID-19

- Literature based probabilities of outcomes with appropriate delays
- Varying levels of infectiousness
- Hypothetical treatments for future developments

ABM Social Distancing Rebound Study Design

Study of ”Stay Home” policy adherence

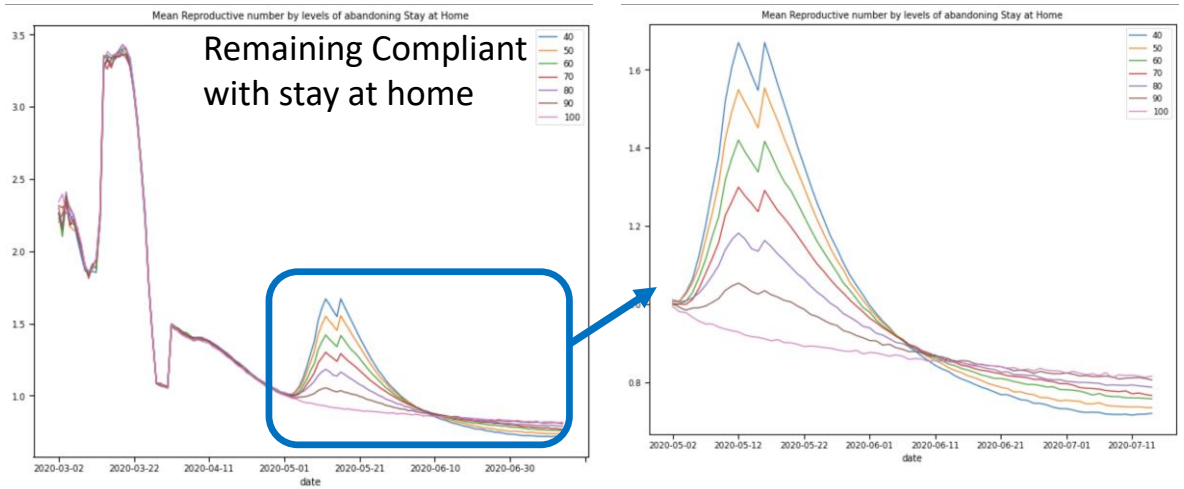
- Calibration to current state in epidemic
- Implement “release” of different proportions of people from ”staying at home”



	date	best case	best guess	worst case	R
1	2020-05-10	664	852	1079	0.95
2	2020-05-17	666	841	1093	0.91
3	2020-05-24	617	768	1111	0.80
4	2020-05-31	547	705	1064	NA

Calibration to Current State

- Adjust transmission and adherence to current policies to current observations
- For Virginia, with same seeding approach as PatchSim



Impacts on Reproductive number with release

- After release, spike in transmission driven by additional interactions at work, retail, and other
- At 25% release (70-80% remain compliant)
- Translates to 15% increase in transmission, which represents a 1/6th return to pre-pandemic levels